

09/765555

-key Terms

(FILE 'HCAPLUS' ENTERED AT 15:40:47 ON 26 MAR 2003)

L1 2551 SEA FILE=HCAPLUS ABB=ON PLU=ON (ZN OR ZINC) (W) FINGER (W) PROTEIN OR ZFP?

L2 153 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 AND (PLANT OR MAIZE OR CORN OR CARROT OR TOBACCO OR TOMATO OR POTATO OR BANANA OR SOYABEAN OR SOYBEAN OR (SOY OR SOYA) (W) BEAN OR PEPPER OR WHEAT OR RYE OR RICE OR SPINACH)

L3 60 SEA FILE=HCAPLUS ABB=ON PLU=ON L2 AND (CELL OR PROTOPLAST? OR SPHEROPLAST? OR (PROTO OR SPHERO) (W) PLAST?)

L4 18 SEA FILE=HCAPLUS ABB=ON PLU=ON L3 AND (ORGANELLE OR MITOCHONDR? OR NUCLEUS OR NUCLEI OR PLASTID OR VACUOLE)

L4 ANSWER 1 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2003:133983 HCAPLUS

DOCUMENT NUMBER: 138:182057

TITLE: Usage of **zinc finger proteins** and their fusions with effector domains to regulate gene expression and metabolic pathways in **plants**

INVENTOR(S): Barbas, Carlos F.; Stege, Justin T.; Guan, Xueni; Dalmia, Bipin

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 84 pp., Cont.-in-part of U.S. Ser. No. 620,897.
CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003037355	A1	20030220	US 2001-765555	20010119
PRIORITY APPLN. INFO.:			US 2000-177468P	P 20000121
			US 2000-620897	A2 20000721

AB The invention relates to the field of **plant** and agricultural technol. More specifically, the invention relates to the construction of **zinc finger proteins** and fusions of said proteins and their use to regulate gene expression and metabolic pathways in **plants**. **Plant** genes AP3 and MIPS were examd. for suitable zinc finger binding sites. The novel engineered **zinc finger proteins** used in the present methods are **ZFPm1, ZFPm2, ZFPm3, ZFPm4** and **ZFPAp3**. These proteins can be used alone or fused to an effector domain. The present methods can be used to modulate gene expression in monocot or dicot **plant cells**.

L4 ANSWER 2 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:900280 HCAPLUS

DOCUMENT NUMBER: 138:168168

TITLE: Mutations in PHF6 are associated with Borjeson-Forssman-Lehmann syndrome

AUTHOR(S): Lower, Karen M.; Turner, Gillian; Kerr, Bronwyn A.; Mathews, Katherine D.; Shaw, Marie A.; Gedeon, Agi K.; Schelley, Susan; Hoyme, H. Eugene; White, Susan M.; Delatycki, Martin B.;

641-8208
300

09/765555

Lampe, Anne K.; Clayton-Smith, Jill; Stewart, Helen; van Ravenswaay, Conny M. A.; de Vries, Bert B. A.; Cox, Barbara; Grompe, Markus; Ross, Shelley; Thomas, Paul; Mulley, John C.; Gecz, Jozef

CORPORATE SOURCE: Centre for Medical Genetics, Department of Cytogenetics and Molecular Genetics, Women's and Children's Hospital, North Adelaide, 5006, Australia

SOURCE: Nature Genetics (2002), 32(4), 661-665
CODEN: NGENEC; ISSN: 1061-4036

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Borjeson-Forssman-Lehmann syndrome (BFLS; OMIM 301900) is characterized by moderate to severe mental retardation, epilepsy, hypogonadism, hypometabolism, obesity with marked gynecomastia, swelling of s.c. tissue of the face, narrow palpebral fissure and large but not deformed ears. Previously, the gene assocd. with BFLS was localized to 17 Mb in Xq26-q27. The authors have reduced this interval to roughly 9 Mb contg. more than 62 genes. Among these, a novel, widely expressed zinc-finger (**plant** homeodomain (PHD)-like finger) gene (PHF6) had eight different missense and truncation mutations in seven familial and two sporadic cases of BFLS. Transient transfection studies with PHF6 tagged with green fluorescent protein (GFP) showed diffuse nuclear staining with prominent nucleolar accumulation. Such localization, and the presence of two PHD-like zinc fingers, is suggestive of a role for PHF6 in transcription.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:833496 HCAPLUS

DOCUMENT NUMBER: 137:347488

TITLE: A method of modulation of endogenous gene expression in **cells** using recombinant **zinc finger proteins** (**ZFPs**)

INVENTOR(S): Case, Casey C.; Wolffe, Alan; Urnov, Fyodor; Lai, Albert; Snowden, Andrew; Tan, Siyuan; Gregory, Philip

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 51 pp., Cont.-in-part of U.S. Ser. No. 229,037.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 6

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002160940	A1	20021031	US 2001-942087	20010828
US 6534261	B1	20030318	US 1999-229037	19990112
JP 2001231583	A2	20010828	JP 2001-5820	20000106
GB 2348424	A1	20001004	GB 2000-650	20000112

Searcher : Shears 308-4994

09/765555

GB 2348424 B2 20010314
US 2002081614 A1 20020627 US 2001-925796 20010809
PRIORITY APPLN. INFO.: US 1999-229037 A2 19990112
US 1999-229007 A 19990112
US 1999-395448 A1 19990914

AB The present application demonstrates for the first time that **zinc finger proteins (ZFPs)** can be used to regulate expression of an endogenous cellular gene that is present in its native chromatin environment. Disclosed herein are methods and compns. for modulating expression of endogenous cellular genes using recombinant **ZFPs**. The method comprises the step of contacting a first target site in the endogenous cellular gene with a designed or selected **ZFP**, and further contacting a second target site in the endogenous cellular gene with a second **ZFP**. The first and second target sites can be adjacent or non-adjacent. Addnl., the first and second **zinc finger proteins** can be covalently linked. The first and/or second **zinc finger protein** can be a fusion protein comprising at least two regulatory domains, or bifunctional domains. Design and testing of **ZFPs** targeted to the human VEGF promoter were demonstrated. Repression and activation of human VEGF-A gene expression using combination of functional domains were also demonstrated. Also the development of expression vectors for producing **ZFPs** within mammalian cells, translocating them to the **nucleus**, and providing functional domains that are localized to the target DNA sequence by the **ZFP** were described. The functional domains employed are the Kruppel-Assocd. Box (KRAB) repression domain and the Herpes Simplex Virus (HSV-1) VP16 activation domain.

L4 ANSWER 4 OF 18 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:120669 HCAPLUS
DOCUMENT NUMBER: 136:307392
TITLE: Moonlighting functions of polypeptide elongation factor 1: from actin bundling to **zinc finger protein** R1-associated nuclear localization
AUTHOR(S): Ejiri, Shin-Ichiro
CORPORATE SOURCE: Cryobiosystem Research Center (CRC), Faculty of Agriculture, Iwate University, Morioka, 020-8550, Japan
SOURCE: Bioscience, Biotechnology, and Biochemistry (2002), 66(1), 1-21
CODEN: BBBIEJ; ISSN: 0916-8451
PUBLISHER: Japan Society for Bioscience, Biotechnology, and Agrochemistry
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. Eukaryotic polypeptide elongation factor EF-1 is not only a major translational factor, but also one of the most important multi-functional (moonlighting) proteins. EF-1 consists of four different subunits collectively termed EF-1.alpha..beta..gamma.'.delta. and EF-1.beta..gamma..delta. in **plants** and animals, resp. EF-1.beta..beta.'.gamma..cntdot.GTP catalyzes the binding of aminoacyl-tRNA to the A-site of the ribosome. EF-1.beta..beta.'.gamma. (EF-1.beta. and EF-1.beta.'), catalyzes GDP/GTP exchange on EF-1.alpha..cntdot.GDP to regenerate

Searcher : Shears 308-4994

EF-1.alpha..cntdot.GTP. EF-1.gamma. has recently been shown to have glutathione S-transferase activity. EF-2 catalyzes the translocation of peptidyl-tRNA from the A-site to the P-site on the ribosome. Recently, mol. mimicry among tRNA, elongation factors, releasing factor (RF), and ribosome recycling factor (RRF) has been demonstrated and greatly improved our understanding of the mechanism of translation. Moreover, eukaryotic elongation factors have been shown to be concerned or likely to be concerned in various important cellular processes or serious diseases, including translational control, signal transduction, cytoskeletal organization, apoptosis, adult atopic dermatitis, oncogenic transformation, nutrition, and nuclear processes such as RNA synthesis and mitosis. This article aims to overview the recent advances in protein biosynthesis, concg. on the moonlighting functions of EF-1.

REFERENCE COUNT: 176 THERE ARE 176 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:107522 HCAPLUS

DOCUMENT NUMBER: 136:162370

TITLE: cDNA and protein sequences of novel polypeptides comprising a 3'-5' exonuclease domain and methods of controlling gene expression and gene silencing in **plants**

INVENTOR(S): Levin, Joshua Zvi; Phillips, Kenneth Lyon; Budziszewski, Gregory Joseph; Meins, Frederick, Jr.; Glazov, Evgueni Alexandrovich

PATENT ASSIGNEE(S): Syngenta Participations A.-G., Switz.; Novartis Forschungsstiftung, Zweigniederlassung Friedrich Miescher Institute for Biomedical Research; Meins, Frederick Jr.

SOURCE: PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002010362	A2	20020207	WO 2001-EP8825	20010730
WO 2002010362	C2	20020919		
WO 2002010362	A3	20030130		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-222202P P 20000801

AB The present invention relates to methods to regulate gene expression in **plants**. In particular, manipulation of the expression

in a **plant cell** of a nucleotide sequence encoding a polypeptide comprising a 3'-5' exonuclease domain is disclosed. More stable and predictable expression is thus obtained. The present invention also relates to method of increasing or decreasing port-transcriptional silencing. The invention further relates to novel nucleic acid mols. comprising nucleotide sequences encoding polypeptides comprising a 3'-5' exonuclease domain.

L4 ANSWER 6 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:86335 HCAPLUS

DOCUMENT NUMBER: 137:16304

TITLE: A. thaliana TRANSPARENT TESTA 1 is involved in seed coat development and defines the WIP subfamily of **plant zinc finger proteins**

AUTHOR(S): Sagasser, Martin; Lu, Gui-Hua; Hahlbrock, Klaus; Weisshaar, Bernd

CORPORATE SOURCE: Max-Planck-Institut fur Zuchtungsforchung Abteilung Biochemie, Koln, D-50829, Germany

SOURCE: Genes & Development (2002), 16(1), 138-149
CODEN: GEDEEP; ISSN: 0890-9369

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Seeds of the Arabidopsis thaliana transparent testa 1 mutant (ttl1) appear yellow, due to the lack of condensed tannin pigments in the seed coat. The TT1 gene was isolated by reverse genetics using an En-1 transposon mutagenized A. thaliana population. TT1 gene expression was detected in developing ovules and young seeds only, and the gene was shown to encode a nuclear protein. Mutant seeds displayed altered morphol. of the seed endothelium in which brown tannin pigments accumulate in wild-type **plants**, indicating that TT1 is involved in the differentiation of this **cell** layer. When overexpressed in transgenic A. thaliana **plants**, TT1 caused aberrant development and organ morphol. The protein contains a novel combination of two TFIIIA-type zinc finger motifs. Closely related motifs were detected in a no. of putative proteins deduced from **plant** genomic and EST sequences. The new protein domain contg. this type of zinc finger motifs was designated WIP, according to three strictly conserved amino acid residues. Our data indicate the existence of a small gene family in A. thaliana which is defined by the occurrence of the WIP domain. WIP genes may play important roles in regulating developmental processes, including the control of endothelium differentiation.

REFERENCE COUNT: 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 7 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:884437 HCAPLUS

DOCUMENT NUMBER: 136:164167

TITLE: The VERNALIZATION 2 gene mediates the epigenetic regulation of vernalization in Arabidopsis

AUTHOR(S): Gendall, Anthony R.; Levy, Yaron Y.; Wilson, Allison; Dean, Caroline

CORPORATE SOURCE: Department of Cell and Developmental Biology, John Innes Centre, Norwich, NR4 7UH, UK

SOURCE: Cell (Cambridge, MA, United States) (2001),

09/765555

107(4), 525-535
CODEN: CELLB5; ISSN: 0092-8674
PUBLISHER: Cell Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The acceleration of flowering by a long period of low temp., vernalization, is an adaptation that ensures **plants** overwinter before flowering. Vernalization induces a developmental state that is mitotically stable, suggesting that it may have an epigenetic basis. The VERNALIZATION2 (VRN2) gene mediates vernalization and encodes a nuclear-localized **zinc finger protein** with similarity to Polycomb group (PcG) proteins of **plants** and animals. In wild-type Arabidopsis, vernalization results in the stable redn. of the levels of the floral repressor FLC. In vrn2 mutants, FLC expression is downregulated normally in response to vernalization, but instead of remaining low, FLC mRNA levels increase when **plants** are returned to normal temps. VRN2 function therefore stably maintains FLC repression after a cold treatment, serving as a mechanism for the cellular memory of vernalization.

REFERENCE COUNT: 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 8 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:829555 HCAPLUS

DOCUMENT NUMBER: 136:99342

TITLE: Cold accumulation of SCOF-1 transcripts is associated with transcriptional activation and mRNA stability

AUTHOR(S): Kim, Jong Cheol; Jeong, Jae Cheol; Park, Hyeong Cheol; Yoo, Jae Hyuk; Koo, Yoon Duck; Yoon, Hae Won; Koo, Sung Chul; Lee, Sung-Ho; Bahk, Jeong Dong; Cho, Moo Je

CORPORATE SOURCE: Division of Applied Life Science (BK 21 program), Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju, 660-701, S. Korea
SOURCE: Molecules and Cells (2001), 12(2), 204-208
CODEN: MOCEEK; ISSN: 1016-8478

PUBLISHER: Springer-Verlag Singapore Pte. Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Cold acclimation enhances the transcription of several cold regulated (COR) genes. However, little is known about whether the elevation of the transcriptional level of the COR genes is due to transcriptional activation, or mRNA stability by a low temp. Recently, we cloned a novel cold-inducible **zinc finger protein** gene from **soybean**, SCOF-1, which may function as a pos. regulator of the COR gene expression. Here we report that the elevation of the SCOF-1 transcript level by cold stress is assocd. with both transcriptional activation and post-transcriptional mRNA stability under a low temp. A nuclear run-on assay reveals that cold acclimation elevates the SCOF-1 transcript about three-fold compared to that of non-acclimated **soybean nuclei**. Furthermore, SCOF-1 transcripts increased substantially by a low temp. in transgenic **tobacco plants** that constitutively

expressed SCOF-1 under the control of a constitutive cauliflower mosaic virus (CaMV) 35S promoter. When a transcription inhibitor, cordycepin, was treated with the deacclimating **soybean cell**, the decay level of the SCOF-1 transcripts was delayed significantly. This suggests that it may affect de novo protein synthesis, which degrades the SCOF-1 mRNA at room temp. In addn., a secondary structure may be involved in the mRNA stability of SCOF-1 under a low temp.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 9 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:803301 HCAPLUS

DOCUMENT NUMBER: 136:304910

TITLE: HUA1, a regulator of stamen and carpel identities in Arabidopsis, codes for a nuclear RNA binding protein

AUTHOR(S): Li, Junjie; Jia, Dongxuan; Chen, Xuemei

CORPORATE SOURCE: Waksman Institute, Rutgers University, Piscataway, NJ, 08854, USA

SOURCE: Plant Cell (2001), 13(10), 2269-2281

CODEN: PLCEEW; ISSN: 1040-4651

PUBLISHER: American Society of Plant Biologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Stamen and carpel identities are specified by the combinatorial activities of several floral homeotic genes, APETALA3, PISTILLATA, AGAMOUS (AG), SEPALLATA1 (SEP1), SEPALLATA2 (SEP2), and SEPALLATA3 (SEP3), all of which code for MADS domain DNA binding proteins. AG and the SEP genes also control floral determinacy. HUA1 and HUA2 were identified previously as regulators of stamen and carpel identities and floral determinacy because the recessive hua1-1 or hua2-1 allele affected these processes in **plants** with a lower dosage of functional AG (either homozygous for the weak ag-4 allele or heterozygous for the strong ag-1 allele). HUA2 was cloned previously and shown to code for a novel protein. We isolated the HUA1 gene using a map-based approach and show that it encodes a protein with six CCCH-type zinc finger motifs that is also found in yeast, Caenorhabditis elegans, Drosophila melanogaster, and mammalian proteins. Several such genes from invertebrates and mammals are known to play key regulatory roles in development. Therefore, HUA1 are another example of non-MADS domain proteins involved in organ identity specification. We demonstrated that HUA1 binds ribohomopolymers, preferentially poly rU and poly rG, but not double-stranded DNA in vitro. This finding suggests that HUA1, like several mammalian CCCH **zinc finger proteins**, is an RNA binding protein. Therefore, HUA1 likely participates in a new regulatory mechanism governing flower development.

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 10 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:545852 HCAPLUS

DOCUMENT NUMBER: 135:148210

TITLE: Engineered **zinc finger**

proteins and their use in regulating
gene expression in **plants**
INVENTOR(S): Choo, Yen; Ullman, Christopher Graeme; Chua,
Nam; Sanchez, Juan Pablo
PATENT ASSIGNEE(S): Gendaq Limited, UK; Rockefeller University
SOURCE: PCT Int. Appl., 61 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001053478	A2	20010726	WO 2001-US2051	20010122
WO 2001053478	A3	20020221		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 2002046419	A1	20020418	US 2000-732348	20001207
PRIORITY APPLN. INFO.:			GB 2000-1578	A 20000124
			US 2000-732348	A 20001207
			GB 1999-12635	A 19990528
			WO 2000-GB2071	A2 20000530

AB The invention provides a method of regulating transcription in a **plant cell** by introducing non-naturally occurring engineered **zinc finger proteins** that confer specificity on gene regulation for both target endogenous genes and transgenes. The **zinc finger proteins** of the invention can be used to up-regulate or down-regulate any gene in the **plant**. The provided chimeric protein is a transcription factor that comprises a DNA binding domain (comprising a no. of zinc finger peptides) designed to bind specifically to any DNA sequence and one or more further domains. Usually, a nuclear localization domain is attached to the DNA binding domain to direct the chimera to the **nucleus**, and generally, the protein also includes an effector domain that can be a transactivation or repression domain to regulate the expression of the target gene.

L4 ANSWER 11 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:545414 HCAPLUS

DOCUMENT NUMBER: 135:133107

TITLE: Usage of **zinc finger protein** to regulate gene expression and metabolic pathways in **plants** and creation of five **zinc finger proteins**

INVENTOR(S): Barbas, Carlos F., III; Stege, Justin T.; Guan, Xue Ni; Dalmia, Bipin

PATENT ASSIGNEE(S): Scripps Research Institute, USA

SOURCE: PCT Int. Appl., 156 pp.

09/765555

CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001052620	A2	20010726	WO 2001-US1817	20010119
WO 2001052620	A3	20020207		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001029641	A5	20010731	AU 2001-29641	20010119
EP 1276869	A2	20030122	EP 2001-942508	20010119
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
PRIORITY APPLN. INFO.:			US 2000-177468P	P 20000121
			US 2000-620897	A 20000721
			WO 2001-US1817	W 20010119

AB The invention relates to the field of **plant** and agricultural technol. More specifically, the invention relates to the use of **zinc finger proteins** and fusions of said proteins to regulate gene expression and metabolic pathways in **plants**. The genes, AP3 and MIPS, were examd. for suitable zinc finger binding sites. Five new **zinc finger proteins**, ZFPap3, ZFPm1, ZFPm2, ZFPm3 and ZFPm4, were constructed from human **zinc finger protein** SplC, expressed in E. coli and purified. DNA binding specificity of ZFPap3, ZFPm1, ZFPm2, ZFPm3 and ZFPm4 was characterized.

L4 ANSWER 12 OF 18 HCAPLUS COPYRIGHT 2003 ACS
 ACCESSION NUMBER: 2001:338762 HCAPLUS
 DOCUMENT NUMBER: 134:362292
 TITLE: Methods of determining individual hypersensitivity to a pharmaceutical agent from gene expression profile
 INVENTOR(S): Farr, Spencer
 PATENT ASSIGNEE(S): Phase-1 Molecular Toxicology, USA
 SOURCE: PCT Int. Appl., 222 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001032928	A2	20010510	WO 2000-US30474	20001103
WO 2001032928	A3	20020725		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,				

Searcher : Shears 308-4994

09/765555

CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG

PRIORITY APPLN. INFO.:

US 1999-165398P P 19991105
US 2000-196571P P 20000411

AB The invention discloses methods, gene databases, gene arrays, protein arrays, and devices that may be used to det. the hypersensitivity of individuals to a given agent, such as drug or other chem., in order to prevent toxic side effects. In one embodiment, methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes assocd. with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes assocd. with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes assocd. with hypersensitivity. The expression of the genes predetd. to be assocd. with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and app. useful for identifying hypersensitivity in a subject are also disclosed.

L4 ANSWER 13 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:312024 HCAPLUS

DOCUMENT NUMBER: 135:340138

TITLE: A genome approach to **mitochondrial**
-nuclear communication in Arabidopsis

AUTHOR(S): Yu, Jianping; Nickels, Roxy; McIntosh, Lee

CORPORATE SOURCE: MSU-DOE Plant Research Laboratory, Michigan
State University, East Lansing, MI, 48824, USA

SOURCE: Plant Physiology and Biochemistry (Paris,
France) (2001), 39(3-4), 345-353

CODEN: PPBIEX; ISSN: 0981-9428

PUBLISHER: Editions Scientifiques et Medicales Elsevier

DOCUMENT TYPE: Journal

LANGUAGE: English

AB **Mitochondria** depend on the nuclear genome to encode the vast majority of their proteins; in turn they control the expression of certain nuclear genes to maintain proper functioning. In this work, Arabidopsis leaves were employed as a model to study nuclear gene expression in response to inhibition of the **mitochondrial** electron transport by antimycin A. Microarrays contg. 11 514 Arabidopsis expressed sequence tags supplied through the Arabidopsis Functional Genomics Consortium (AFGC) were used. Transcript levels of 579 nuclear genes were increased .gtoreq. 2-fold, and the levels of 584 nuclear genes were decreased .gtoreq. 2-fold after antimycin A treatment. While

functions of a large no. of the gene products are unknown, others are involved in diverse metabolic activities such as phosphorylation, transcription, and energy metab. Data from microarray expts. were repeatable and were confirmed by northern hybridization for specific test genes. It was found through cluster anal. that **plant cells** show significant common response to chem. inhibition of **mitochondrial** function, aluminum stress, cadmium stress, hydrogen peroxide and virus infection. The results imply that these stresses may act on **mitochondria** and the responses are in part mediated by **mitochondrial-nuclear** communication. Most nuclear-encoded respiratory genes involved in the TCA cycle, electron transport and ATP synthesis did not respond to signals from the inhibited **mitochondria**, while genes for cytochrome c and alternative oxidase were induced. The result indicates that these two genes may be targets in the transcriptional regulation of the two respiratory pathways.

REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 14 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:236491 HCAPLUS

DOCUMENT NUMBER: 135:31301

TITLE: A novel cold-inducible **zinc finger protein** from **soybean**, SCOF-1, enhances cold tolerance in transgenic **plants**

AUTHOR(S): Kim, Jong Cheol; Lee, Sang Hyoung; Cheong, Yong Hwa; Yoo, Cheol-Min; Lee, Soo In; Chun, Hyun Jin; Yun, Dae-Jin; Hong, Jong Chan; Lee, Sang Yeol; Lim, Chae Oh; Cho, Moo Je

CORPORATE SOURCE: Division of Applied Life Science, Gyeongsang National University, Jinju, 660-701, S. Korea

SOURCE: Plant Journal (2001), 25(3), 247-259

CODEN: PLJUED; ISSN: 0960-7412

PUBLISHER: Blackwell Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Cold stress on **plants** induces changes in the transcription of cold response genes. A cDNA clone encoding C2H2-type **zinc finger protein**, SCOF-1, was isolated from **soybean**. The transcription of SCOF-1 is specifically induced by low temp. and abscisic acid (ABA) but not by dehydration or high salinity. Constitutive overexpression of SCOF-1 induced cold-regulated (COR) gene expression and enhanced cold tolerance of non-acclimated transgenic Arabidopsis and **tobacco plants**. SCOF-1 localized to the **nucleus** but did not bind directly to either C-repeat/dehydration (CRT/DRE) or ABA responsive element (ABRE), cis-acting DNA regulatory elements present in COR gene promoters. However, SCOF-1 greatly enhanced the DNA binding activity of SGBF-1, a **soybean** G-box binding bZIP transcription factor, to ABRE in vitro. SCOF-1 also interacted with SGBF-1 in a yeast two-hybrid system. The SGBF-1 transactivated the .beta.-glucuronidase reporter gene driven by the ABRE element in Arabidopsis leaf **protoplasts**. Furthermore, the SCOF-1 enhanced ABRE-dependent gene expression mediated by SGBF-1. These results

suggest that SCOF-1 may function as a pos. regulator of COR gene expression mediated by ABRE via protein-protein interaction, which in turn enhances cold tolerance of **plants**.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 15 OF 18 HCAPLUS COPYRIGHT 2003 ACS
 ACCESSION NUMBER: 2001:228746 HCAPLUS
 DOCUMENT NUMBER: 134:261836
 TITLE: Cell based assay for signal transduction comprising chimeric ligand-inducible transcription factors and its therapeutic application
 INVENTOR(S): Zhong, Zhong; Kelly, Glen L.; Mercolino, Thomas J.; Zivin, Robert; Siekierka, John J.
 PATENT ASSIGNEE(S): Ortho-McNeil Pharmaceutical, Inc., USA
 SOURCE: PCT Int. Appl., 53 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001021215	A1	20010329	WO 2000-US25314	20000915
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1218036	A1	20020703	EP 2000-965037	20000915
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
JP 2003509078	T2	20030311	JP 2001-524638	20000915
PRIORITY APPLN. INFO.: US 1999-155353P P 19990922				
WO 2000-US25314 W 20000915				

AB The present invention provides a whole-cell biol. assay that measures changes of endogenous genes under control of an exogenously introduced transcription factor. The exogenous transcription factors of the present invention may be designed such that each is activated by specific extracellular ligands. Therefore **cells** contg. exogenous transcription factors of the present invention provide a generic means to which many extracellular ligands may be tested without undue adaptation to the assay. The invention is exemplified by measuring estradiol induction of EPO protein gene under the control of specific promoters mediated by a chimeric zinc finger transcription factor **ZFP-ERLBD** contg. ligand binding domain and transcription activation domain from estrogen receptor 1.alpha. and DNA binding domain specific to EPO protein gene promoter. Transcription factor compns. related to interferon (IFN) signaling involved with Jak-STAT receptor pathway,

09/765555

dopamine signaling involved with G protein-coupled receptor, and PDGF signaling involved with receptor tyrosine kinase pathway are also described. The method can be used for drug screening or analyzing drug effects.

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 16 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2000:595882 HCAPLUS

DOCUMENT NUMBER: 133:277781

TITLE: Characterization of a novel gene encoding a putative single **zinc-finger protein**, ZIM, expressed during the reproductive phase in *Arabidopsis thaliana*

AUTHOR(S): Nishi, Akiko; Takemura, Miho; Fujita, Hidetomo; Shikata, Masahito; Yokota, Akiho; Kohchi, Takayuki

CORPORATE SOURCE: Graduate School of Biological Sciences, Nara Institute of Science and Technology, Nara, 630-0101, Japan

SOURCE: Bioscience, Biotechnology, and Biochemistry (2000), 64(7), 1402-1409
CODEN: BBBIEJ; ISSN: 0916-8451

PUBLISHER: Japan Society for Bioscience, Biotechnology, and Agrochemistry

DOCUMENT TYPE: Journal

LANGUAGE: English

AB By differential screening of an arrayed normalized cDNA library from the inflorescence apex in *Arabidopsis*, a cDNA clone having a deduced amino acid sequence with a motif for a zinc finger was isolated as one of the genes expressed specifically in the reproductive phase. The deduced protein has a modular structure with a putative single C2-C2 zinc-finger motif distantly related to a GATA-1-type finger, a basic region with a sequence resembling a nuclear localization signal, and an acidic region. The gene seemed to have been formed by the exon-shuffling during its mol. evolution, since individual domains are encoded by discrete exons. RNA gel blot anal. showed its expression in shoot apex and flowers in the reproductive phase. The gene was named ZIM for **Zinc-finger protein** expressed in Inflorescence Meristem. The nuclear localization of ZIM was detected using GFP as a reporter. These results suggest that ZIM is a putative transcription factor involved in inflorescence and lower development.

REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 17 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:87508 HCAPLUS

DOCUMENT NUMBER: 128:226993

TITLE: Involvement of **maize Dof zinc finger proteins** in tissue-specific and light-regulated gene expression

AUTHOR(S): Yanagisawa, Shuichi; Sheen, Jen

CORPORATE SOURCE: Department of Life Sciences (Chemistry), Graduate School of Arts and Sciences, University

SOURCE: of Tokyo, Tokyo, 153, Japan
 Plant Cell (1998), 10(1), 75-89
 CODEN: PLCEEW; ISSN: 1040-4651

PUBLISHER: American Society of Plant Physiologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Dof is a novel family of **plant** proteins that share a unique and highly conserved DNA binding domain with one C2-C2 zinc finger motif. Although multiple Dof proteins assocd. with diverse gene promoters have recently been identified in a variety of **plants**, their physiol. functions and regulation remain elusive. In **maize**, Dof1 (MNB1a) is constitutively expressed in leaves, stems, and roots, whereas the closely related Dof2 is expressed mainly in stems and roots. Here, by using a **maize** leaf **protoplast** transient assay, we show that Dof1 is a transcriptional activator, whereas Dof2 can act as a transcriptional repressor. Thus, differential expression of Dof1 and Dof2 may permit leaf-specific gene expression. Interestingly, in vivo analyses showed that although DNA binding activity of Dof1 is regulated by light-dependent development, its transactivation activity and nuclear localization are not. Moreover, in vivo transcription and in vitro electrophoretic mobility shift assays revealed that Dof1 can interact specifically with the **maize** C4 phosphoenolpyruvate carboxylase gene promoter and enhance its promoter activity, which displays a light-regulated expression pattern matching Dof1 activity. We propose that the evolutionarily conserved Dof proteins can function as transcriptional activators or repressors of tissue-specific and light-regulated gene expression in **plants**.

L4 ANSWER 18 OF 18 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1995:694101 HCAPLUS

DOCUMENT NUMBER: 123:139066

TITLE: Molecular analysis of chloroplast division

AUTHOR(S): Reski, R.; Reutter, K.; Kasten, B.; Faust, M.; Kruse, S.; Gorr, G.; Strepp, R.; Abel, W. O.

CORPORATE SOURCE: Institute General Botany, University Hamburg, Hamburg, 22609, Germany

SOURCE: Current Plant Science and Biotechnology in Agriculture (1995), 22(Current Issues in Plant Molecular and Cellular Biology), 291-6
 CODEN: CPBAE2; ISSN: 0924-1949

PUBLISHER: Kluwer

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The mol. events underlying chloroplast division are studied with a mutant of a moss, *Physcomitrella patens*, which is defective in chloroplast division thus possessing one giant lobed chloroplast per **cell**. This macrochloroplast is severed by the enlarging **cell** plate during cytokinesis. Its division can be induced by cytokinin and by blue light. Concomitantly, maturation of complex **plastid** transcripts and a transient occurrence of **plastid** polypeptides can be detected. Southern-analyses revealed methylation of the mutants **plastid** DNA around an open reading frame (ORF), possibly encoding a **zinc-finger protein**. This ORF is conserved from cyanobacteria to the **plastids** of archegoniates but is absent from the **plastid** DNA of monocots. Somatic

hybridization were performed to allocate the mutations either to nuclear or to **plastid** DNA. Four cytokinin-modulated cDNAs representing novel genes were isolated by mol. subtraction. Transformants with the bacterial ipt-gene were generated, one of which has lost sensitivity towards cytokinin and blue light in the chloroplast division process.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CABA, AGRICOLA, FSTA, CROPU, CROPB' ENTERED AT 15:46:24 ON 26 MAR 2003)

L5 44 S L4
L6 36 DUP REM L5 (8 DUPLICATES REMOVED)

L6 ANSWER 1 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2003037562 EMBASE
TITLE: Two RNA binding proteins, HEN4 and HUA1 act in the processing of AGAMOUS pre-mRNA in Arabidopsis thaliana.
AUTHOR: Cheng Y.; Kato N.; Wang W.; Li J.; Chen X.
CORPORATE SOURCE: X. Chen, Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854, United States. xuemei@waksman.rutgers.edu
SOURCE: Developmental Cell, (1 Jan 2003) 4/1 (53-66).
Refs: 62
ISSN: 1534-5807 CODEN: DCEEBE
PUBLISHER IDENT.: S 1534-5807(02)00399-4
COUNTRY: United States
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB AGAMOUS, a key player in floral morphogenesis, specifies reproductive organ identities and regulates the timely termination of stem **cell** fates in the floral meristem. Here, we report that strains carrying mutations in three genes, HUA1, HUA2, and HUA ENHANCER4 (HEN4), exhibit floral defects similar to those in agamous mutants: reproductive-to-perianth organ transformation and loss of floral determinacy. HEN4 codes for a K homology (KH) domain-containing, putative RNA binding protein that interacts with HUA1, a CCCH zinc finger RNA binding protein in the **nucleus**. We show that HUA1 binds AGAMOUS pre-mRNA in vitro and that HEN4, HUA1, and HUA2 act in floral morphogenesis by specifically promoting the processing of AGAMOUS pre-mRNA. Our studies under-score the importance of RNA processing in modulating **plant** development.

L6 ANSWER 2 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2002207310 EMBASE
TITLE: LOS2, a genetic locus required for cold-responsive gene transcription encodes a bi-functional enolase.
AUTHOR: Hojoung L.; Guo Y.; Ohta M.; Xiong L.; Stevenson B.; Zhu J.-K.
CORPORATE SOURCE: J.-K. Zhu, Department of Plant Sciences, University of Arizona, Tucson, AZ 85721, United States. jkzhu@ag.arizona.edu
SOURCE: EMBO Journal, (3 Jun 2002) 21/11 (2692-2702).
Refs: 29
ISSN: 0261-4189 CODEN: EMJODG

COUNTRY: United Kingdom
 DOCUMENT TYPE: Journal; Article
 FILE SEGMENT: 029 Clinical Biochemistry
 LANGUAGE: English
 SUMMARY LANGUAGE: English

AB The Arabidopsis mutation, *los2*, impairs cold-responsive gene transcription, acquired freezing tolerance and **plant** resistance to chilling under certain conditions. *LOS2* was isolated through positional cloning and shown to encode an enolase in the glycolytic pathway. In animal **cells**, enolase has also been known to function as a transcription factor that represses the expression of *c-myc* by binding to the *c-myc* gene promoter. *LOS2* fused to green fluorescent protein is targeted to the **nucleus** as well as to the cytoplasm. *LOS2/enolase* protein can bind to the *cis*-element of the human *c-myc* gene promoter and to the gene promoter of *STZ/ZAT10*, a zinc finger transcriptional repressor from Arabidopsis. *STZ/ZAT10* expression is induced rapidly and transiently by cold in the wild type, and this induction is stronger and more sustained in the *los2* mutant. Furthermore, the expression of a *RD29A-LUC* reporter gene is repressed significantly by *STZ/ZAT10* in transient expression assays in Arabidopsis leaves. Our results demonstrate that cold-responsive gene transcription in **plants** is controlled by a bi-functional enolase.

L6 ANSWER 3 OF 36 SCISEARCH COPYRIGHT 2003 ISI (R)
 ACCESSION NUMBER: 2002:660402 SCISEARCH
 THE GENUINE ARTICLE: 578RF
 TITLE: Molecular genetic analysis of cold-regulated gene transcription
 AUTHOR: Viswanathan C; Zhu J K (Reprint)
 CORPORATE SOURCE: Univ Arizona, Dept Plant Sci, Tucson, AZ 85721 USA (Reprint)
 COUNTRY OF AUTHOR: USA
 SOURCE: PHILOSOPHICAL TRANSACTIONS OF THE ROYAL SOCIETY OF LONDON SERIES B-BIOLOGICAL SCIENCES, (29 JUL 2002) Vol. 357, No. 1423, pp. 877-886.
 Publisher: ROYAL SOC LONDON, 6 CARLTON HOUSE TERRACE, LONDON SW1Y 5AG, ENGLAND.
 ISSN: 0962-8436.
 DOCUMENT TYPE: Article; Journal
 LANGUAGE: English
 REFERENCE COUNT: 86

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Chilling and freezing temperatures adversely affect the productivity and quality of crops. Hence improving the cold hardiness of crop **plants** is an important goal in agriculture, which demands a clear understanding of cold stress signal perception and transduction. Pharmacological and biochemical evidence shows that membrane rigidification followed by cytoskeleton rearrangement, Ca^{2+} influx and Ca^{2+} -dependent phosphorylation are involved in cold stress signal transduction. Cold-responsive genes are regulated through C-repeat/dehydration-responsive elements (CRT/DRE) and abscisic acid (ABA)-responsive element *cis*-elements by transacting factors C-repeat binding factors/dehydration-responsive element binding proteins (CBFs/DREBs) and basic, leucine zippers (bZIPs) (SGBF1), respectively. We have carried out a forward genetic analysis using chemically mutagenized Arabidopsis **plants** expressing cold-responsive *RD29A* promoter-driven luciferase to

dissect cold signal transduction. We have isolated the fiery1 (fry1) mutant and cloned the FRY1 gene, which encodes an inositol polyphosphate 1-phosphatase. The fry1 **plants** showed enhanced induction of stress genes in response to cold, ABA, salt and dehydration due to higher accumulation of the second messenger, inositol (1,4,5)- triphosphate (IP3). Thus our study provides genetic evidence suggesting that cold signal is transduced through changes in IP3 levels. We have also identified the hos1 mutation, which showed super induction of cold-responsive genes and their transcriptional activators. Molecular cloning and characterization revealed that HOS1 encodes a ring finger protein, which has been implicated as an E3 ubiquitin conjugating enzyme. HOS1 is present in the cytoplasm at normal growth temperatures but accumulates in the **nucleus** upon cold stress. HOS1 appears to regulate temperature sensing by the **cell** as cold-responsive gene expression occurs in the hos1 mutant at relatively warm temperatures. Thus HOS1 is a negative regulator, which may be functionally linked to cellular thermosensors to modulate cold-responsive gene transcription.

L6 ANSWER 4 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:385223 BIOSIS
 DOCUMENT NUMBER: PREV200200385223
 TITLE: Zinc-dependent intermembrane space proteins stimulate import of carrier proteins into **plant mitochondria**.
 AUTHOR(S): Lister, Ryan; Mowday, Brett; Whelan, James; Millar, A. Harvey (1)
 CORPORATE SOURCE: (1) Plant Molecular Biology Group, School of Biomedical and Chemical Sciences, The University of Western Australia, Crawley, WA, 6009: hmillar@cyllene.uwa.edu.au Australia
 SOURCE: Plant Journal, (June, 2002) Vol. 30, No. 5, pp. 555-566. <http://www.blackwell-science.com/cgilib/jnlpage.bin?Journal=TPJ&File=TPJ&Page=aims.print>.
 ISSN: 0960-7412.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB **Mitochondrial** inner membrane carrier proteins are imported into **mitochondria** from yeast, fungi and mammals by specific machinery, some components of which are distinct from those utilized by other proteins. Import of two different carriers into **plant mitochondria** showed that one contains a cleavable presequence which was processed during import, while the other imported in a valinomycin-sensitive manner without processing. Mild osmotic shock of **mitochondria** released intermembrane space (IMS) components and impaired carrier protein import. Adding back the released IMS proteins as a concentrate in the presence of micromolar ZnCl2 stimulated carrier import into IMS-depleted **mitochondria**, but did not stimulate import of a non-carrier control precursor protein, the alternative oxidase. Anion-exchange separation of IMS components before addition to IMS-depleted **mitochondria** revealed a correlation between several 9-10 kDa proteins and stimulation of carrier import. MS/MS sequencing of these proteins identified them as **plant** homologues of the yeast zinc-finger carrier import components Tim9 and Tim10. Stimulation of import was dependent on either Zn2+ or Cd2+ and

inhibited by both N-ethylmaleimide (NEM) and a divalent cation chelator, consistent with a functional requirement for a **zinc finger protein**. This represents direct functional evidence for a distinct carrier import pathway in **plant mitochondria**, and provides a tool for determining the potential function of other IMS proteins associated with protein import.

L6 ANSWER 5 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:298175 BIOSIS
 DOCUMENT NUMBER: PREV200200298175
 TITLE: Yeast Npi3/Bro1 is involved in ubiquitin-dependent control of permease trafficking.
 AUTHOR(S): Springael, Jean-Yves; Nikko, Elina; Andre, Bruno (1); Marini, Anne-Marie
 CORPORATE SOURCE: (1) Laboratoire de Physiologie Cellulaire, Institut de Biologie et de Medecine Moleculaires, Universite Libre de Bruxelles, Rue des Professeurs Jeener et Brachet 12, 6041, Gosselies: bran@ulb.ac.be Belgium
 SOURCE: FEBS Letters, (24 April, 2002) Vol. 517, No. 1-3, pp. 103-109. <http://www.elsevier.com/febs>. print.
 ISSN: 0014-5793.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB The membrane traffic and stability of the general amino acid permease Gap1 of *Saccharomyces cerevisiae* are under nitrogen control. Addition of a preferential nitrogen source such as ammonium to **cells** growing on a poor nitrogen source induces internalization of the permease and its subsequent degradation in the **vacuole**. This down-regulation requires ubiquitination of Gap1 through a process involving ubiquitin ligase Npi1/Rsp5, ubiquitin hydrolase Npi2/Doa4, and Bull2, two Npi1/Rsp5 interacting proteins. Here we report that yet another protein, Npi3, is involved in the regulation of Gap1 trafficking. We show that Npi3 is required for NH₄⁺-induced down-regulation of Gap1, and particularly for efficient ubiquitination of the permease. Npi3 plays a pleiotropic role in permease down-regulation, since it is also involved in ubiquitination and stress-induced down-regulation of the uracil permease Fur4 and in glucose-induced degradation of hexose transporters Hxt6/7. We further provide evidence that Npi3 is required for direct vacuolar sorting of neosynthesized Gap1 permease as it occurs in *npr1* mutant **cells**. NPI3 is identical to BRO1, a gene encoding a protein of unknown biochemical function and recently proposed to be involved in protein turnover. Npi3/Bro1 homologues include fungal proteins required for proteolytic cleavage of **zinc finger proteins** and the mouse Aipl protein involved in apoptosis. We propose that proteins of the Npi3/Bro1 family, including homologues from higher species, may play a conserved role in ubiquitin-dependent control of membrane protein trafficking.

L6 ANSWER 6 OF 36 MEDLINE DUPLICATE 1
 ACCESSION NUMBER: 2002130634 MEDLINE
 DOCUMENT NUMBER: 21854920 PubMed ID: 11866090
 TITLE: Moonlighting functions of polypeptide elongation factor 1: from actin bundling to **zinc finger protein** R1-associated nuclear localization.

09/765555

AUTHOR: Ejiri Shin-ichiro
CORPORATE SOURCE: Cryobiosystem Research Center, Faculty of
Agriculture, Iwate University, Morioka, Japan.
SOURCE: BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, (2002
Jan) 66 (1) 1-21. Ref: 176
Journal code: 9205717. ISSN: 0916-8451.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200210
ENTRY DATE: Entered STN: 20020228
Last Updated on STN: 20021008
Entered Medline: 20021004
AB Eukaryotic polypeptide elongation factor EF-1 is not only a major
translational factor, but also one of the most important
multifunctional (moonlighting) proteins. EF-1 consists of four
different subunits collectively termed EF-lalphanbeta beta'gamma and
EF-lalphanbeta gammadelta in **plants** and animals,
respectively. EF-lalpha x GTP catalyzes the binding of
aminoacyl-tRNA to the A-site of the ribosome. EF-lbeta beta'gamma
(EF-lbeta and EF-lbeta'), catalyzes GDP/GTP exchange on EF-lalpha x
GDP to regenerate EF-lalpha x GTP. EF-lgamma has recently been shown
to have glutathione S-transferase activity. EF-2 catalyzes the
translocation of peptidyl-tRNA from the A-site to the P-site on the
ribosome. Recently, molecular mimicry among tRNA, elongation
factors, releasing factor (RF), and ribosome recycling factor (RRF)
has been demonstrated and greatly improved our understanding of the
mechanism of translation. Moreover, eukaryotic elongation factors
have been shown to be concerned or likely to be concerned in various
important cellular processes or serious diseases, including
translational control, signal transduction, cytoskeletal
organization, apoptosis, adult atopic dermatitis, oncogenic
transformation, nutrition, and nuclear processes such as RNA
synthesis and mitosis. This article aims to overview the recent
advances in protein biosynthesis, concentrating on the moonlighting
functions of EF-1.

L6 ANSWER 7 OF 36 WPIDS (C) 2003 THOMSON DERWENT
ACCESSION NUMBER: 2001-465325 [50] WPIDS
DOC. NO. NON-CPI: N2001-345166
DOC. NO. CPI: C2001-140479
TITLE: New **zinc finger**
proteins, useful for modulating or
regulating gene expression and metabolic pathways
in **plants**, e.g. for treating in the
plant cells a disorder that is
associated with abnormal expression of the target
gene.
DERWENT CLASS: C06 D16 P13
INVENTOR(S): BARBAS, C F; DALMIA, B; GUAN, X; STEGE, J T
PATENT ASSIGNEE(S): (SCRI) SCRIPPS RES INST; (TORR-N) TORREY MESA RES
INST; (BARB-I) BARBAS C F; (DALM-I) DALMIA B;
(GUAN-I) GUAN X; (STEG-I) STEGE J T; (SYGN)
SYNGENTA AGRIC DISCOVERY INC
COUNTRY COUNT: 95

Searcher : Shears 308-4994

09/765555

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001052620	A2	20010726	(200150)*	EN	156
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE					
DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG					
KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ					
PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN					
YU ZA ZW					
AU 2001029641	A	20010731	(200171)		
EP 1276869	A2	20030122	(200308)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK					
NL PT RO SE SI TR					
US 2003037355	A1	20030220	(200316)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001052620	A2	WO 2001-US1817	20010119
AU 2001029641	A	AU 2001-29641	20010119
EP 1276869	A2	EP 2001-942508	20010119
		WO 2001-US1817	20010119
US 2003037355	A1 Provisional	US 2000-177468P	20000121
		US 2001-765555	20010119

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2001029641	A Based on	WO 200152620
EP 1276869	A2 Based on	WO 200152620

PRIORITY APPLN. INFO: US 2000-620897 20000721; US 2000-177468P
20000121; US 2001-765555 20010119

AN 2001-465325 [50] WPIDS

AB WO 200152620 A UPAB: 20010905

NOVELTY - A new **zinc finger protein** (**ZFP**) comprises:

(a) zinc finger nucleic acid binding domain and effector domain, the effector contains restriction enzyme domain, a nucleic acid modifying protein active domain, a label or a modification;

(b) **ZFPm1**, **ZFPm2**, **ZFPm3**, **ZFPm4** or **ZFPap3**; or

(c) a **ZFP** that is detected by antibody that binds to (b), or to fusion protein having zinc finger of 2C7 and effector domain of SID3.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method for modulating the expression of a target gene in **plant cells** comprising:

(a) providing **plant cells** with a **zinc finger protein**, which is capable of specifically binding to a target nucleotide sequence or its complementary strand, within a target gene; and

(b) allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant cells is modulated;

(2) a method of modulating a level of a compound in a plant cell comprising expressing in a plant cell a ZFP that specifically binds to a target nucleotide sequence within a target gene to modulate expression of the target gene, which is involved in a compound's metabolism in the plant cell, where level of the compound in the plant cell is modulated;

(3) an expression vector, which comprises a nucleotide sequence encoding a ZFP, for modulating gene expression in plant cells;

(4) genetically modified plant cells:

(a) comprising the expression system for a ZFP;

(b) transformed with a nucleic acid comprising a functional geminiviral replicase gene operably linked to a fruit ripening-dependent promoter;

(c) comprising an exogenous ZFP that specifically binds to a target nucleotide sequence in the plant cell, where the exogenous ZFP is constitutively expressed; or

(d) comprising an exogenous ZFP that specifically binds to a target nucleotide sequence in the plant cell, where the exogenous ZFP is inducibly expressed;

(5) a genetically modified plant tissue comprising the genetically modified plant cell;

(6) genetically modified plant seeds:

(a) comprising the genetically modified plant cells; or

(b) transformed with a nucleic acid having a geminiviral replicase gene operably linked to a fruit ripening-dependent promoter;

(7) a plant that is regenerated from a plant transformed with the expression vector;

(8) an antibody that:

(a) specifically binds to the ZFP; or

(b) specifically binds to a fusion protein having a zinc finger of 2C7 and an effector domain of SID3;

(9) an isolated nucleic acid fragment comprising:

(a) a sequence of nucleotides encoding the ZFP;

(b) a sequence of nucleotides encoding a fusion protein having the zinc finger of 2C7 and an effector domain of SID3; or

(c) a nucleic acid fragment that is hybridizable to (a) or (b);

(10) plasmids comprising the nucleic acid fragments;

(11) cell comprising the plasmids;

(12) a method for producing the ZFP comprising growing the cell, where the ZFP is expressed by the cell, and recovering the expressed zinc finger protein;

(13) an assay method for determining a suitable position in a gene for regulating gene expression in plant cells comprising:

(a) providing a target gene, which contains a nucleotide sequence encoding a reporter protein within the coding region of the target gene and a target nucleotide sequence at a predetermined location within the target gene;

(b) contacting the target gene with a regulatory factor comprising a ZFP specific for the target nucleotide sequence; and

(c) assessing the level of expression of the reporter gene in the presence and absence of the contacting; where a change in the level of expression of the reporter gene in the presence as opposed to the absence of the contacting identifies the position of the target nucleotide sequence as a position suitable for controlling expression of the target gene in plant cells;

(14) a fusion protein comprising a zinc finger of 2C7 and an effector domain of SID; and

(15) a method for producing the fusion protein comprising growing the cell so the fusion protein is expressed by the cell, and recovering the expressed fusion protein.

USE - The ZFP and fusions of the proteins is useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene.

Dwg.0/24

L6 ANSWER 8 OF 36 MEDLINE
 ACCESSION NUMBER: 2001549428 MEDLINE
 DOCUMENT NUMBER: 21480067 PubMed ID: 11595801
 TITLE: HUA1, a regulator of stamen and carpel identities in Arabidopsis, codes for a nuclear RNA binding protein.
 AUTHOR: Li J; Jia D; Chen X
 CORPORATE SOURCE: Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, New Jersey 08854, USA.
 CONTRACT NUMBER: GM61146-02 (NIGMS)
 SOURCE: PLANT CELL, (2001 Oct) 13 (10) 2269-81.
 Journal code: 9208688. ISSN: 1040-4651.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AY024357
 ENTRY MONTH: 200201
 ENTRY DATE: Entered STN: 20011015
 Last Updated on STN: 20020129
 Entered Medline: 20020128

AB Stamen and carpel identities are specified by the combinatorial activities of several floral homeotic genes, APETALA3, PISTILLATA, AGAMOUS (AG), SEPALLATA1 (SEP1), SEPALLATA2 (SEP2), and SEPALLATA3 (SEP3), all of which code for MADS domain DNA binding proteins. AG and the SEP genes also control floral determinacy. HUA1 and HUA2 were identified previously as regulators of stamen and carpel identities and floral determinacy because the recessive hua1-1 or hua2-1 allele affected these processes in **plants** with a lower dosage of functional AG (either homozygous for the weak ag-4 allele or heterozygous for the strong ag-1 allele). HUA2 was cloned previously and shown to code for a novel protein. We isolated the HUA1 gene using a map-based approach and show that it encodes a protein with six CCCH-type zinc finger motifs that is also found in yeast, *Caenorhabditis elegans*, *Drosophila melanogaster*, and mammalian proteins. Several such genes from invertebrates and mammals are known to play key regulatory roles in development. Therefore, HUA1 are another example of non-MADS domain proteins involved in organ identity specification. We demonstrated that HUA1

binds ribohomopolymers, preferentially poly rU and poly rG, but not double-stranded DNA in vitro. This finding suggests that HUA1, like several mammalian CCCH **zinc finger proteins**, is an RNA binding protein. Therefore, HUA1 likely participates in a new regulatory mechanism governing flower development.

L6 ANSWER 9 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:355229 BIOSIS
 DOCUMENT NUMBER: PREV200100355229
 TITLE: Interaction of the repressors Nrg1 and Nrg2 with the Snf1 protein kinase in *Saccharomyces cerevisiae*.
 AUTHOR(S): Vyas, Valmik K.; Kuchin, Sergei; Carlson, Marian (1)
 CORPORATE SOURCE: (1) Columbia University, 701 W. 168th St., HSC922, New York, NY, 10032: mbcl@columbia.edu USA
 SOURCE: Genetics, (June, 2001) Vol. 158, No. 2, pp. 563-572. print.
 ISSN: 0016-6731.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English
 AB The Snf1 protein kinase is essential for the transcription of glucose-repressed genes in *Saccharomyces cerevisiae*. We identified Nrg2 as a protein that interacts with Snf1 in the two-hybrid system. Nrg2 is a C2H2 **zinc-finger protein** that is homologous to Nrg1, a repressor of the glucose- and Snf1-regulated STA1 (glucoamylase) gene. Snf1 also interacts with Nrg1 in the two-hybrid system and co-immunoprecipitates with both Nrg1 and Nrg2 from **cell** extracts. A LexA fusion to Nrg2 represses transcription from a promoter containing LexA binding sites, indicating that Nrg2 also functions as a repressor. An Nrg1 fusion to green fluorescent protein is localized to the **nucleus**, and this localization is not regulated by carbon source. Finally, we show that VP16 fusions to Nrg1 and Nrg2 allow low-level expression of SUC2 in glucose-grown **cells**, and we present evidence that Nrg1 and Nrg2 contribute to glucose repression of the DOG2 gene. These results suggest that Nrg1 and Nrg2 are direct or indirect targets of the Snf1 kinase and function in glucose repression of a subset of Snf1-regulated genes.

L6 ANSWER 10 OF 36 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2001408918 MEDLINE
 DOCUMENT NUMBER: 21157266 PubMed ID: 11208017
 TITLE: A novel cold-inducible **zinc finger protein** from **soybean**, SCOF-1, enhances cold tolerance in transgenic **plants**.
 AUTHOR: Kim J C; Lee S H; Cheong Y H; Yoo C M; Lee S I; Chun H J; Yun D J; Hong J C; Lee S Y; Lim C O; Cho M J
 CORPORATE SOURCE: Division of Applied Life Science, Gyeongsang National University, Chinju 660-701, Korea.
 SOURCE: PLANT JOURNAL, (2001 Feb) 25 (3) 247-59.
 Journal code: 9207397. ISSN: 0960-7412.
 PUB. COUNTRY: England: United Kingdom
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200107

09/765555

ENTRY DATE: Entered STN: 20010723
 Last Updated on STN: 20010723
 Entered Medline: 20010719

AB Cold stress on **plants** induces changes in the transcription of cold response genes. A cDNA clone encoding C2H2-type **zinc finger protein**, SCOF-1, was isolated from **soybean**. The transcription of SCOF-1 is specifically induced by low temperature and abscisic acid (ABA) but not by dehydration or high salinity. Constitutive overexpression of SCOF-1 induced cold-regulated (COR) gene expression and enhanced cold tolerance of non-acclimated transgenic Arabidopsis and **tobacco plants**. SCOF-1 localized to the **nucleus** but did not bind directly to either C-repeat/dehydration (CRT/DRE) or ABA responsive element (ABRE), cis-acting DNA regulatory elements present in COR gene promoters. However, SCOF-1 greatly enhanced the DNA binding activity of SGBF-1, a **soybean** G-box binding bZIP transcription factor, to ABRE in vitro. SCOF-1 also interacted with SGBF-1 in a yeast two-hybrid system. The SGBF-1 transactivated the beta-glucuronidase reporter gene driven by the ABRE element in Arabidopsis leaf **protoplasts**. Furthermore, the SCOF-1 enhanced ABRE-dependent gene expression mediated by SGBF-1. These results suggest that SCOF-1 may function as a positive regulator of COR gene expression mediated by ABRE via protein-protein interaction, which in turn enhances cold tolerance of **plants**.

L6 ANSWER 11 OF 36 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001664701 MEDLINE
DOCUMENT NUMBER: 21566750 PubMed ID: 11710522
TITLE: Cold accumulation of SCOF-1 transcripts is associated with transcriptional activation and mRNA stability.
AUTHOR: Kim J C; Jeong J C; Park H C; Yoo J H; Koo Y D; Yoon H W; Koo S C; Lee S H; Bahk J D; Cho M J
CORPORATE SOURCE: Division of Applied Life Science, Gyeongsang National University, Chinju, Korea.
SOURCE: MOLECULES AND CELLS, (2001 Oct 31) 12 (2) 204-8.
Journal code: 9610936. ISSN: 1016-8478.
PUB. COUNTRY: Korea (South)
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20011119
Last Updated on STN: 20020514
Entered Medline: 20020513

AB Cold acclimation enhances the transcription of several cold regulated (COR) genes. However, little is known about whether the elevation of the transcriptional level of the COR genes is due to transcriptional activation, or mRNA stability by a low temperature. Recently, we cloned a novel cold-inducible **zinc finger protein** gene from **soybean**, SCOF-1, which may function as a positive regulator of the COR gene expression. Here we report that the elevation of the SCOF-1 transcript level by cold stress is associated with both transcriptional activation and post-transcriptional mRNA stability under a low temperature. A nuclear run-on assay reveals that cold acclimation elevates the SCOF-1 transcript about three-fold compared to that of non-acclimated **soybean nuclei**.

Searcher : Shears 308-4994

Furthermore, SCOF-1 transcripts increased substantially by a low temperature in transgenic **tobacco plants** that constitutively expressed SCOF-1 under the control of a constitutive cauliflower mosaic virus (CaMV) 35S promoter. When a transcription inhibitor, cordycepin, was treated with the deacclimating **soybean cell**, the decay level of the SCOF-1 transcripts was delayed significantly. This suggests that it may affect de novo protein synthesis, which degrades the SCOF-1 mRNA at room temperature. In addition, a secondary structure may be involved in the mRNA stability of SCOF-1 under a low temperature.

L6 ANSWER 12 OF 36 MEDLINE
 ACCESSION NUMBER: 2001051423 MEDLINE
 DOCUMENT NUMBER: 20399353 PubMed ID: 10945256
 TITLE: Characterization of a novel gene encoding a putative single **zinc-finger protein**, ZIM, expressed during the reproductive phase in *Arabidopsis thaliana*.
 AUTHOR: Nishii A; Takemura M; Fujita H; Shikata M; Yokota A; Kohchi T
 CORPORATE SOURCE: Graduate School of Biological Sciences, Nara Institute of Science and Technology, Ikoma, Japan.
 SOURCE: BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, (2000 Jul) 64 (7) 1402-9.
 Journal code: 9205717. ISSN: 0916-8451.
 PUB. COUNTRY: Japan
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB035310
 ENTRY MONTH: 200012
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001212
 AB By differential screening of an arrayed normalized cDNA library from the inflorescence apex in *Arabidopsis*, a cDNA clone having a deduced amino acid sequence with a motif for a zinc finger was isolated as one of the genes expressed specifically in the reproductive phase. The deduced protein has a modular structure with a putative single C2-C2 zinc-finger motif distantly related to a GATA-1-type finger, a basic region with a sequence resembling a nuclear localization signal, and an acidic region. The gene seemed to have been formed by the exon-shuffling during its molecular evolution, since individual domains are encoded by discrete exons. RNA gel blot analysis showed its expression in shoot apex and flowers in the reproductive phase. The gene was named ZIM for **Zinc-finger protein** expressed in Inflorescence Meristem. The nuclear localization of ZIM was detected using GFP as a reporter. These results suggest that ZIM is a putative transcription factor involved in inflorescence and flower development.

L6 ANSWER 13 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
 ACCESSION NUMBER: 2000149651 EMBASE
 TITLE: Stimulated apoptosis as an anti-neoplastic strategy.
 AUTHOR: Arya J.; Finlayson C.A.; Shames B.D.; Harken A.H.; Anderson B.O.
 CORPORATE SOURCE: Dr. J. Arya, Department of Surgery (C-305), Univ. of Colorado Hlth. Sci. Center, 4200 E Ninth Ave, Denver,

09/765555

SOURCE: CO 80262, United States
Surgery, (2000) 127/4 (366-369).
Refs: 39
ISSN: 0039-6060 CODEN: SURGAZ
COUNTRY: United States
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 009 Surgery
016 Cancer
026 Immunology, Serology and Transplantation
030 Pharmacology
037 Drug Literature Index
LANGUAGE: English

L6 ANSWER 14 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1999:299775 BIOSIS

DOCUMENT NUMBER: PREV199900299775

TITLE: MHY1 encodes a C2H2-type zinc
finger protein that promotes
dimorphic transition in the yeast *Yarrowia*
lipolytica.

AUTHOR(S): Hurtado, Cleofe A.R.; Rachubinski, Richard A. (1)

CORPORATE SOURCE: (1) Department of Cell Biology, University of
Alberta, Medical Sciences Building 5-14, Edmonton,
Alberta, T6G 2H7 Canada

SOURCE: Journal of Bacteriology, (May, 1999) Vol. 181, No.
10, pp. 3051-3057.
ISSN: 0021-9193.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

AB The yeast-to-hypha morphological transition (dimorphism) is typical
of many pathogenic fungi. Dimorphism has been attributed to changes
in temperature and nutritional status and is believed to constitute
a mechanism of response to adverse conditions. We have isolated and
characterized a gene, MHY1, whose transcription is dramatically
increased during the yeast-to-hypha transition in *Yarrowia*
lipolytica. Deletion of MHY1 is viable and has no effect on mating,
but it does result in a complete inability of **cells** to
undergo mycelial growth. MHY1 encodes a C2H2-type zinc
finger protein, Mhy1p, which can bind putative
cis-acting DNA stress response elements, suggesting that Mhy1p may
act as a transcription factor. Interestingly, Mhy1p tagged with a
hemagglutinin epitope was concentrated in the **nuclei** of
actively growing **cells** found at the hyphal tip.

L6 ANSWER 15 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1999:166832 BIOSIS

DOCUMENT NUMBER: PREV199900166832

TITLE: A novel genetic screen for snRNP assembly factors in
yeast identifies a conserved protein, Sad1p, also
required for pre-mRNA splicing.

AUTHOR(S): Lygerou, Zoi; Christophides, George; Seraphin,
Bertrand (1)

CORPORATE SOURCE: (1) EMBL, Meyerhofstrasse 1, 69117 Heidelberg Germany

SOURCE: Molecular and Cellular Biology, (March, 1999) Vol.
19, No. 3, pp. 2008-2020.
ISSN: 0270-7306.

DOCUMENT TYPE: Article

Searcher : Shears 308-4994

LANGUAGE: English

AB The assembly pathway of spliceosomal snRNPs in yeast is poorly understood. We devised a screen to identify mutations blocking the assembly of newly synthesized U4 snRNA into a functional snRNP. Fifteen mutant strains failing either to accumulate the newly synthesized U4 snRNA or to assemble a U4/U6 particle were identified and categorized into 13 complementation groups. Thirteen previously identified splicing-defective prp mutants were also assayed for U4 snRNP assembly defects. Mutations in the U4/U6 snRNP components Prp3p, Prp4p, and Prp24p led to disassembly of the U4/U6 snRNP particle and degradation of the U6 snRNA, while prp17-1 and prp19-1 strains accumulated free U4 and U6 snRNA. A detailed analysis of a newly identified mutant, the sad1-1 mutant, is presented. In addition to having the snRNP assembly defect, the sad1-1 mutant is severely impaired in splicing at the restrictive temperature: the RP29 pre-mRNA strongly accumulates and splicing-dependent production of beta-galactosidase from reporter constructs is abolished, while extracts prepared from sad1-1 strains fail to splice pre-mRNA substrates in vitro. The sad1-1 mutant is the only splicing-defective mutant analyzed whose mutation preferentially affects assembly of newly synthesized U4 snRNA into the U4/U6 particle. SAD1 encodes a novel protein of 52 kDa which is essential for cell viability. Sad1p localizes to the nucleus and is not stably associated with any of the U snRNAs. Sad1p contains a putative zinc finger and is phylogenetically highly conserved, with homologues identified in human, Caenorhabditis elegans, Arabidopsis, and Drosophila.

L6 ANSWER 16 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 1999158893 EMBASE

TITLE: Cloning of the APECED gene provides new insight into human autoimmunity.

AUTHOR: Aaltonen J.; Bjorses P.

CORPORATE SOURCE: Dr. P. Bjorses, National Public Health Institute, Department Human Molecular Genetics, Mannerheimintie 166, FIN-00300 Helsinki, Finland.
petra.bjorses@ktl.fi

SOURCE: Annals of Medicine, (1999) 31/2 (111-116).

Refs: 41

ISSN: 0785-3890 CODEN: ANMDEU

COUNTRY: United Kingdom

DOCUMENT TYPE: Journal; (Short Survey)

FILE SEGMENT: 005 General Pathology and Pathological Anatomy

022 Human Genetics

026 Immunology, Serology and Transplantation

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Autoimmune polyendocrinopathy-candidiasis-ectoderm dystrophy (APECED) is the only autoimmune disease characterized so far that is caused by a defect in a single gene. We have recently isolated the defective gene in this disease by positional cloning and have identified several different mutations in APECED patients. This novel gene, AIRE, contains two plant homeodomain (PHD)-type zinc finger motifs and a newly described putative DNA-binding domain SAND. We have further shown that the protein encoded by the AIRE gene is localized to the nuclear body-like structures of cell nuclei. Similar discrete speckles within the nucleus have been suggested to be

involved in the regulation of transcription, oncogenesis and differentiation of **cells**. Together with the predicted structural features of the APECED protein the new data obtained both in vitro and ex vivo suggest that this protein participates in the regulation of gene expression in a restricted set of tissues and **cells**.

L6 ANSWER 17 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
 ACCESSION NUMBER: 1998307092 EMBASE
 TITLE: HRT, a novel zinc finger, transcriptional repressor from barley.
 AUTHOR: Raventos D.; Skriver K.; Schlein M.; Karnahl K.; Rogers S.W.; Rogers J.C.; Mundy J.
 CORPORATE SOURCE: J. Mundy, Molecular Biology Institute, Copenhagen University, Oster Farimagsgade 2A, 1353 Copenhagen K, Denmark. mundy@biobase.dk
 SOURCE: Journal of Biological Chemistry, (4 Sep 1998) 273/36 (23313-23320).
 Refs: 47
 ISSN: 0021-9258 CODEN: JBCHA3
 COUNTRY: United States
 DOCUMENT TYPE: Journal; Article
 FILE SEGMENT: 029 Clinical Biochemistry
 LANGUAGE: English
 SUMMARY LANGUAGE: English

AB A barley gene encoding a novel DNA-binding protein (HRT) was identified by southwestern screening with baits containing a gibberellin phytohormone response element from an .alpha.-amylase promoter. The HRT gene contains two introns, the larger of which (5722 base pairs (bp)) contains a 3094-bp LINE- like element with homology to **maize** Colonist1. In vitro mutagenesis and zinc- and DNA-binding assays demonstrate that HRT contains three unusual zinc fingers with a CX8-9CX10CX2H consensus sequence. HRT is targeted to **nuclei**, and homologues are expressed in other **plants**. In vivo, functional tests in **plant cells** indicate that full-length HRT can repress expression from certain promoters including the Amy1[6-4 and Amy2/32 .alpha.-amylase promoters. In contrast, truncated forms of HRT containing DNA-binding domains can activate, or derepress, transcription from these promoters. Northern hybridizations indicate that HRT mRNA accumulates to low levels in various tissues. Roles for HRT in mediating developmental and phytohormone- responsive gene expression are discussed.

L6 ANSWER 18 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1999:57753 BIOSIS
 DOCUMENT NUMBER: PREV199900057753
 TITLE: Interaction of ZPR1 with translation elongation factor-1alpha in proliferating **cells**.
 AUTHOR(S): Gangwani, Laxman; Mikrut, Monique; Galcheva-Gargova, Zoya; Davis, Roger J. (1)
 CORPORATE SOURCE: (1) Howard Hughes Med. Inst., Program Molecular Med., Univ. Massachusetts Med. Sch., 373 Plantation St., Worcester, MA 01605 USA
 SOURCE: Journal of Cell Biology, (Dec. 14, 1998) Vol. 143, No. 6, pp. 1471-1484.
 ISSN: 0021-9525.
 DOCUMENT TYPE: Article

LANGUAGE: English

AB The **zinc finger protein ZPR1** is present in the cytoplasm of quiescent mammalian **cells** and translocates to the **nucleus** upon treatment with mitogens, including epidermal growth factor (EGF). Homologues of ZPR1 were identified in yeast and mammals. These ZPR1 proteins bind to eukaryotic translation elongation factor-lalpha (eEF-lalpha). Studies of mammalian **cells** demonstrated that EGF treatment induces the interaction of ZPR1 with eEF-lalpha and the redistribution of both proteins to the **nucleus**. In the yeast *Saccharomyces cerevisiae*, genetic analysis demonstrated that ZPR1 is an essential gene. Deletion analysis demonstrated that the NH2-terminal region of ZPR1 is required for normal growth and that the COOH-terminal region was essential for viability in *S. cerevisiae*. The yeast ZPR1 protein redistributes from the cytoplasm to the **nucleus** in response to nutrient stimulation. Disruption of the binding of ZPR1 to eEF-lalpha by mutational analysis resulted in an accumulation of **cells** in the G2/M phase of **cell** cycle and defective growth. Reconstitution of the ZPR1 interaction with eEF-lalpha restored normal growth. We conclude that ZPR1 is essential for **cell** viability and that its interaction with eEF-lalpha contributes to normal cellular proliferation.

L6 ANSWER 19 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1998:162852 BIOSIS

DOCUMENT NUMBER: PREV199800162852

TITLE: Nuclear localization of the C2H2 **zinc finger protein Msn2p** is regulated by stress and protein kinase A activity.

AUTHOR(S): Goerner, Wolfram; Durschlag, Erich; Martinez-Pastor, Maria Teresa; Estruch, Francisco; Ammerer, Gustav; Hamilton, Barbara; Ruis, Helmut; Schueller, Christoph (1)

CORPORATE SOURCE: (1) Vienna Biocenter, Inst. Biochemie Mol. Zellbiol., Univ. Wien, A-1030 Wien Austria

SOURCE: Genes & Development, (Feb. 15, 1998) Vol. 12, No. 4, pp. 586-597.
ISSN: 0890-9369.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Msn2p and the partially redundant factor Msn4p are key regulators of stress-responsive gene expression in *Saccharomyces cerevisiae*. They are required for the transcription of a number of genes coding for proteins with stress-protective functions. Both Msn2p and Msn4p are Cys2His2 **zinc finger proteins** and bind to the stress response element (STRE). In vivo footprinting studies show that the occupation of STREs is enhanced in stressed **cells** and dependent on the presence of Msn2p and Msn4p. Both factors accumulate in the **nucleus** under stress conditions, such as heat shock, osmotic stress, carbon-source starvation, and in the presence of ethanol or sorbate. Stress-induced nuclear localization was found to be rapid, reversible, and independent of protein synthesis. Nuclear localization of Msn2p and Msn4p was shown to be correlated inversely to cAMP levels and protein kinase A (PKA) activity. A region with significant homologies shared between Msn2p and Msn4p is sufficient to confer stress-regulated localization to a SV40-NLS-GFP fusion protein. Serine to alanine or aspartate

substitutions in a conserved PKA consensus site abolished cAMP-driven nuclear export and cytoplasmic localization in unstressed **cells**. We propose stress and cAMP-regulated intracellular localization of Msn2p to be a key step in STRE-dependent transcription and in the general stress response.

L6 ANSWER 20 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1999:35530 BIOSIS

DOCUMENT NUMBER: PREV199900035530

TITLE: Azflp is a nuclear-localized **zinc-finger protein** that is preferentially expressed under non-fermentative growth conditions in *Saccharomyces cerevisiae*.

AUTHOR(S): Stein, Torsten; Kricke, Joern; Becher, Dietmar; Lisowsky, Thomas (1)

CORPORATE SOURCE: (1) Botanisches Inst. I, Heinrich-Heine-Univ. Duesseldorf, Universitaetsstrasse 1, D-40225 Duesseldorf Germany

SOURCE: Current Genetics, (Oct., 1998) Vol. 34, No. 4, pp. 287-296.
ISSN: 0172-8083.

DOCUMENT TYPE: Article

LANGUAGE: English

AB In previous studies the AZF1 gene has been identified as a second high-copy number suppressor for a special mutant of the gene for the **mitochondrial** core enzyme of RNA polymerase. The first high-copy number suppressor of this mutant turned out to be the specificity factor MTF1 for **mitochondrial** transcription. Up to now, the influence of AZF1 on **mitochondrial** transcription, its precise localization in the **cell** and the regulation of its expression has not been determined. The putative protein contains a long stretch of poly-asparagine amino acids and a typical zinc-finger domain for DNA binding. These characteristic structural features were used to create the abbreviation AZF1 (A sparagine-rich **Zinc Finger protein**). An initial computer analysis of the sequence gave no conclusive results for the presence of a **mitochondrial** import sequence or a typical nuclear-targeting sequence. A recent more-detailed analysis identified a possible nuclear localization signal in the middle of the protein. Disruption of the gene shows no effect on plates with glucose-rich medium or glycerol. In this report a specific polyclonal antibody against AZF1 p was prepared and used in **cell**-fractionation experiments and in electron-microscopic studies. Both of these clearly demonstrate that the AZF1 protein is localized exclusively in the **nucleus** of the yeast **cell**. Northern analysis for the expression of the AZF1 messenger RNA under different growth conditions was therefore performed to obtain new insights into the regulation of this gene. Together with the respective protein-expression analysis these data demonstrate that Azflp is preferentially synthesized in higher amounts under non-fermentable growth conditions. Over-expression of Azflp in the yeast **cell** does not influence the expression level of the **mitochondrial** transcription factor Mtf1p, indicating that the influence of Azflp on the suppression of the special **mitochondrial** RNA polymerase mutant is an indirect one. Subcellular investigation of the deletion mutant by electron microscopy identifies specific ultrastructural **cell**-division defects in comparison to the

wild-type.

L6 ANSWER 21 OF 36 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 1998138060 MEDLINE
 DOCUMENT NUMBER: 98138060 PubMed ID: 9477573
 TITLE: Involvement of **maize** Dof zinc
finger proteins in tissue-specific
 and light-regulated gene expression.
 AUTHOR: Yanagisawa S; Sheen J
 CORPORATE SOURCE: Department of Life Sciences (Chemistry), Graduate
 School of Arts and Sciences, University of Tokyo,
 Japan.. ccyanag@komaba.ecc.u-tokyo.ac.jp
 SOURCE: PLANT CELL, (1998 Jan) 10 (1) 75-89.
 Journal code: 9208688. ISSN: 1040-4651.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199804
 ENTRY DATE: Entered STN: 19980422
 Last Updated on STN: 19980422
 Entered Medline: 19980413

AB Dof is a novel family of **plant** proteins that share a
 unique and highly conserved DNA binding domain with one C2-C2 zinc
 finger motif. Although multiple Dof proteins associated with diverse
 gene promoters have recently been identified in a variety of
plants, their physiological functions and regulation remain
 elusive. In **maize**, Dof1 (MNBl1) is constitutively
 expressed in leaves, stems, and roots, whereas the closely related
 Dof2 is expressed mainly in stems and roots. Here, by using a
maize leaf **protoplast** transient assay, we show
 that Dof1 is a transcriptional activator, whereas Dof2 can act as a
 transcriptional repressor. Thus, differential expression of Dof1 and
 Dof2 may permit leaf-specific gene expression. Interestingly, in
 vivo analyses showed that although DNA binding activity of Dof1 is
 regulated by light-dependent development, its transactivation
 activity and nuclear localization are not. Moreover, in vivo
 transcription and in vitro electrophoretic mobility shift assays
 revealed that Dof1 can interact specifically with the **maize**
 C4 phosphoenolpyruvate carboxylase gene promoter and enhance its
 promoter activity, which displays a light-regulated expression
 pattern matching Dof1 activity. We propose that the evolutionarily
 conserved Dof proteins can function as transcriptional activators or
 repressors of tissue-specific and light-regulated gene expression in
plants.

L6 ANSWER 22 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1997:450569 BIOSIS
 DOCUMENT NUMBER: PREV199799749772
 TITLE: Regulated nuclear translocation of the Mig1 glucose
 repressor.
 AUTHOR(S): Devit, Michael J.; Waddle, James A.; Johnston, Mark
 (1)
 CORPORATE SOURCE: (1) Dep. Genetics, Box 8232, Washington Univ. Sch.
 Med., 660 South Euclid Ave., St. Louis, MO 63110 USA
 SOURCE: Molecular Biology of the Cell, (1997) Vol. 8, No. 8,
 pp. 1603-1618.
 ISSN: 1059-1524.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Glucose represses the transcription of many genes in bakers yeast (*Saccharomyces cerevisiae*). Mig1 is a CYS2-His-2 **zinc finger protein** that mediates glucose repression of several genes by binding to their promoters and recruiting the general repression complex Ssn6-Tup1. We have found that the subcellular localization of Mig1 is regulated by glucose. Mig1 is imported into the **nucleus** within minutes after the addition of glucose and is just as rapidly transported back to the cytoplasm when glucose is removed. This regulated nuclear localization requires components of the glucose repression signal transduction pathway. An internal region of the protein separate from the DNA binding and repression domains is necessary and sufficient for glucose-regulated nuclear import and export. Changes in the phosphorylation status of Mig1 are coincident with the changes in its localization, suggesting a possible regulatory role for phosphorylation. Our results suggest that a glucose-regulated nuclear import and/or export mechanism controls the activity of Mig1.

L6 ANSWER 23 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 97272615 EMBASE

DOCUMENT NUMBER: 1997272615

TITLE: Cloning and molecular characterization of an *Arabidopsis thaliana* RING zinc finger gene expressed preferentially during seed development.

AUTHOR: Zou J.; Taylor D.C.

CORPORATE SOURCE: D.C. Taylor, National Research Council of Canada, Plant Biotechnology Institute, Seed Oil Modification Group, 110 Gymnasium Place, Saskatoon, Sask. S7N 0W9, Canada. dtaylor@pbi.nrc.ca

SOURCE: Gene, (1997) 196/1-2 (291-295).

Refs: 19

ISSN: 0378-1119 CODEN: GENED6

COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 022 Human Genetics

LANGUAGE: English

SUMMARY LANGUAGE: English

AB The RING (Really Interesting New Gene) finger is a zinc-binding domain that is found in proteins from a variety of species. This paper reports the cloning and characterization of, as yet, only the second RING finger protein gene from **plants**, A-RZF, in *Arabidopsis thaliana*. In addition to the RING-finger motif, A-RZF also contains a putative nuclear localization signal. A-RZF is encoded by a single copy gene with an intron of 595 bp interrupting the 5' leader sequence and the coding region. Northern blot analysis indicated that A-RZF is expressed preferentially during seed development. The RING-finger motif, putative nuclear localization signal, and unique expression pattern, predict an important role during seed development for A-RZF.

L6 ANSWER 24 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1996:313436 BIOSIS

DOCUMENT NUMBER: PREV199699035792

TITLE: Faithful chromosome transmission requires Spt4p, a putative regulator of chromatin structure in

Saccharomyces cerevisiae.
 AUTHOR(S): Basrai, Munira A.; Kingsbury, Jeffrey; Koshland, Douglas; Spencer, Forrest; Hieter, Philip (1)
 CORPORATE SOURCE: (1) Dep. Mol. Biol. Genetics, 725 N. Wolfe St., Hunterian 617, The Johns Hopkins Univ. Sch. Med., Baltimore, MD 21210-2185 USA
 SOURCE: Molecular and Cellular Biology, (1996) Vol. 16, No. 6, pp. 2838-2847.
 ISSN: 0270-7306.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB A chromosome transmission fidelity (ctf) mutant, s138, of Saccharomyces cerevisiae was identified by its centromere (CEN) transcriptional readthrough phenotype, suggesting perturbed kinetochore integrity in vivo. The gene complementing the s138 mutation was found to be identical to the S. cerevisiae SPT4 gene. The s138 mutation is a missense mutation in the second of four conserved cysteine residues positioned similarly to those of **zinc finger proteins**, and we henceforth refer to the mutation as spt4-138. Both spt4-138 and spt4-DELTA strains missegregate a chromosome fragment at the permissive temperature, are temperature sensitive for growth at 37 degree C, and upon a shift to the nonpermissive temperature show an accumulation of large budded **cells**, each with a **nucleus**. Previous studies suggest that Spt4p functions in a complex with Spt5p and Spt6p, and we determined that spt6-140 also causes missegregation of a chromosome fragment. Double mutants carrying spt4-DELTA-2:: HIS3 and kinetochore mutation ndc10-42 or ctf13-30 show a synthetic conditional phenotype. Both spt4-138 and spt4-DELTA strains exhibit synergistic chromosome instability in combination with CEN DNA mutations and show in vitro defects in microtubule binding to minichromosomes. These results indicate that Spt4p plays a role in chromosome segregation. The results of in vivo genetic interactions with mutations in kinetochore proteins and CEN DNA and of in vitro biochemical assays suggest that Spt4p is important for kinetochore function.

L6 ANSWER 25 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1996:194078 BIOSIS
 DOCUMENT NUMBER: PREV199698750207
 TITLE: Asymmetric accumulation of Ash1p in postanaphase

nuclei depends on a myosin and restricts yeast mating-type switching to mother **cells**

AUTHOR(S): Bobola, Nicoletta; Jansen, Ralf-Peter; Shin, Tae Ho; Nasmyth, Kim
 CORPORATE SOURCE: Research Inst. Molecular Pathol., A-1030 Vienna Austria
 SOURCE: Cell, (1996) Vol. 84, No. 5, pp. 699-709.
 ISSN: 0092-8674.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB Cell division in haploid yeast gives rise to a "mother" cell capable of mating-type switching and a "daughter" cell that is not. Switching is initiated by the HO endonuclease, whose gene is only transcribed in **cells** that have previously given birth to a bud (mother **cells**). HO expression depends on a minimyosin, Shelp/Myo4p, which accumulates

preferentially in growing buds. We describe a gene, **ASH1**, that is necessary to repress **HO** in daughters. **ASH1** encodes a **zinc finger protein** whose preferential accumulation in daughter **cell nuclei** at the end of anaphase depends on **Shelp/Myo4p**. The greater abundance of **Ash1p** in daughter **cells** is responsible for restricting **HO** expression to mother **cells**.

L6 ANSWER 26 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1995:484515 BIOSIS
 DOCUMENT NUMBER: PREV199598498815
 TITLE: Schizosaccharomyces pombe zfs1+ encoding a **zinc-finger protein** functions in the mating pheromone recognition pathway.
 AUTHOR(S): Kanoh, Junko; Sugimoto, Asako; Yamamoto, Masayuki (1)
 CORPORATE SOURCE: (1) Dep. Biophysics Biochem., Sch. Sci., Univ. Tokyo, Hongo, Tokyo 112 Japan
 SOURCE: Molecular Biology of the Cell, (1995) Vol. 6, No. 9, pp. 1185-1195.
 ISSN: 1059-1524.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB We isolated the Schizosaccharomyces pombe zfs1 gene as a multicopy suppressor of the sterility caused by overexpression of a double-stranded RNase. The deduced zfs1 gene product of 404 amino acids showed similarity to a mouse growth factor-inducible nuclear protein Nup475. Its C-terminal region carried two putative zinc-fingers, both of which should be intact for the protein to be functional as the suppressor. This protein appeared to localize in **nuclei**. Disruption of zfs1 was not lethal but conferred deficiency in mating and sporulation. Activation of transcription in response to mating pheromone signaling was greatly reduced in the zfs1-disrupted **cells**. The mating deficiency of the zfs1-disruptant was suppressed partially by overexpression of either gpa1, ras1, byr1, or byr2, which are involved in the transmission of the pheromone signal. Disruption of zfs1 reduced both hypersensitivity of the ras1-Vall7 mutant to the mating pheromone and uncontrolled mating response caused by mutational activation of Gpa1, the G protein alpha subunit coupled to the mating pheromone receptors. However, overexpression of zfs1 could not bypass complete loss of function of either gpa1, ras1, byr1, or byr2. These observations indicate that the function of zfs1 is involved in the mating pheromone signaling pathway, and are consistent with its function being required to fully activate a factor in this pathway, either directly or indirectly.

L6 ANSWER 27 OF 36 SCISEARCH COPYRIGHT 2003 ISI (R)
 ACCESSION NUMBER: 95:377797 SCISEARCH
 THE GENUINE ARTICLE: RA417
 TITLE: INACTIVATION OF A SYNECHOCYSTIS SP STRAIN PCC-6803 GENE WITH HOMOLOGY TO CONSERVED CHLOROPLAST OPEN READING FRAME-184 INCREASES THE PHOTOSYSTEM-II-TO-PHOTOSYSTEM-I RATIO
 AUTHOR: WILDE A; HARTEL H; HUBSCHMANN T; HOFFMANN P; SHESTAKOV S V; BORNER T (Reprint)
 CORPORATE SOURCE: HUMBOLDT UNIV BERLIN, INST BIOL, INVALIDENSTR 43, D-10115 BERLIN, GERMANY (Reprint); HUMBOLDT UNIV

BERLIN, INST BIOL, D-10115 BERLIN, GERMANY; MOSCOW
 MV LOMONOSOV STATE UNIV, DEPT GENET, MOSCOW 119899,
 RUSSIA
 COUNTRY OF AUTHOR: GERMANY; RUSSIA
 SOURCE: PLANT CELL, (MAY 1995) Vol. 7, No. 5, pp. 649-658.
 ISSN: 1040-4651.
 DOCUMENT TYPE: Article; Journal
 FILE SEGMENT: LIFE; AGRI
 LANGUAGE: ENGLISH
 REFERENCE COUNT: 58

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A gene of the unicellular cyanobacterium *Synechocystis* sp strain PCC 6803 that is homologous to the conserved chloroplast open reading frame orf184 has been cloned and sequenced. The nucleotide sequence of the gene predicts a protein of 184 amino acids with a calculated molecular mass of 21.5 kD and two membrane-spanning regions. Amino acid sequence analysis showed 46 to 37% homology of the cyanobacterial orf184 with **tobacco** orf184, **rice** orf185, liverwort orf184, and *Euglena gracilis* orf206 sequences. Two orf184-specific mutants of *Synechocystis* sp PCC 6803 were constructed by insertion mutagenesis. **Cells** of mutants showed growth characteristics similar to those of the wild type. Their pigment composition was distinctly different from the wild type, as indicated by an increase in the phycocyanin-to-chlorophyll ratio. In addition, mutants also had a two- to threefold increase in photosynthetic electron transfer rates as well as in photosystem II-to-photosystem I ratio-a phenomenon hitherto not reported for mutants with altered photosynthetic characteristics. The observed alterations in the orf184-specific mutants provide strong evidence for a functional role of the orf184 gene product in photosynthetic processes.

L6 ANSWER 28 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1995:157214 BIOSIS
 DOCUMENT NUMBER: PREV199598171514
 TITLE: The yeast homologue YTIS11, of the mammalian TIS11 gene family is a non-essential, glucose repressible gene.
 AUTHOR(S): Ma, Qiufu; Herschman, Harvey R. (1)
 CORPORATE SOURCE: (1) Dep. Biol. Chem., UCLA Center Health Sci., Los Angeles, CA 90024 USA
 SOURCE: Oncogene, (1995) Vol. 10, No. 3, pp. 487-494.
 ISSN: 0950-9232.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB The murine TIS11 primary response gene is rapidly and transiently induced in response to many extracellular signals. A CX-8CX-5CX-3H sequence is present twice in the TIS11 protein, in two additional murine proteins, TIS11B and TIS11D, that share regions of strong sequence conservation with TIS11, and in a *Drosophila* homologue (DTIS11). Although immunolocalization of TIS11 protein to the **nucleus** and zinc binding have lead to the speculation that the TIS11 family proteins are transcription factors, no function for these proteins has yet been clearly determined. We have now identified a TIS11 homologue, YTIS11, from *Saccharomyces cerevisiae*. The Ytis11p protein conserves both the two putative zinc finger CX-8CX-5CX-3H sequences and the spacing between them, as well as additional amino acids in this region. The amino terminal 169 amino

acid portion of Ytis11p protein, which contains a large number of acidic amino acids, can serve as a transactivator when fused to the Gal4 DNA-binding domain. Expression of the YTIS11 gene is not induced in response to DNA damaging agents, heat shock, sporulation conditions, or mating factor. However, YTIS11 expression is subjected to rapid glucose repression. Disruption of the YTIS11 gene in the M12B strain of *Saccharomyces cerevisiae* does not effect viability, growth in rich or synthetic medium, mating, or spore formation. However, YTIS11 gene disruption causes an alteration in metabolism that is reflected by a pH color change when cells are grown on YP plates supplemented with 2% glucose. Overexpression of murine TIS11 or TIS11B proteins dramatically attenuates the growth of both *ytis11* and wild-type yeast.

L6 ANSWER 29 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1995:437971 BIOSIS
 DOCUMENT NUMBER: PREV199598452271
 TITLE: An open reading frame (*ycf11*) is evolutionary conserved from cyanobacteria to the **plastid** DNAs of archegoniates and gymnosperms, is modified in the **plastid** DNAs of dicots, and is not plastome encoded in monocots.
 AUTHOR(S): Kruse, S.; Martin, W.; Wehe, M.; Reski, R. (1)
 CORPORATE SOURCE: (1) Inst. Allgemeine Botanik, Ohnhorstr. 18, 22609 Hamburg Germany
 SOURCE: Journal of Plant Physiology, (1995) Vol. 146, No. 3, pp. 258-262.
 ISSN: 0176-1617.
 DOCUMENT TYPE: Article
 LANGUAGE: English

AB To study molecular evolution of **plants**, the **plastid** encoded *rbcL* sequences are widely used. In most **plastid** DNAs, an open reading frame (ORF) designated *ycf11* can be found next to the highly conserved *rbcL* gene. This ORF appears to be only loosely conserved and its function is a matter of debate: On the one hand it is the only gene in **plastid** DNA of land **plants** suspected to encode a regulatory **zinc finger protein**. On the other hand it was postulated to encode the beta-subunit of an acetyl-CoA-carboxylase. Accordingly, this ORF has been previously described as **zfpA** or *accD*, respectively. Phylogenetic analysis reveals evolutionary conservation of two *ycf11*-domains from bacteria to the **plastids** of dicots. We show that in dicots *ycf11* has gained additional sequences through insertions, whereas it has been lost from the **plastid** DNA in monocots. These findings may reflect physiological differences between major groups of land **plants**. Furthermore, we show that *ycf11* may be a useful molecular marker in the study of **plant** evolution.

L6 ANSWER 30 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1994:358648 BIOSIS
 DOCUMENT NUMBER: PREV199497371648
 TITLE: A new nuclear suppressor system for a **mitochondrial** RNA polymerase mutant identifies an unusual **zinc-finger protein** and a polyglutamine domain protein in *Saccharomyces cerevisiae*.
 AUTHOR(S): Broehl, Stefanie; Lisowsky, Thomas; Riemen, Gudula;

CORPORATE SOURCE: Michaelis, Georg (1)
 (1) Botanisches Inst., Univ. Duesseldorf, Univ. 1,
 D-40225 Duesseldorf Germany
 SOURCE: Yeast, (1994) Vol. 10, No. 6, pp. 719-731.
 ISSN: 0749-503X.

DOCUMENT TYPE: Article

LANGUAGE: English

AB A yeast strain with a point mutation in the nuclear gene for the core subunit of **mitochondrial** RNA polymerase was used to isolate new extragenic suppressors. Spontaneously occurring phenotypical revertants were analysed by crosses with the wild-type and tetrad dissection. One of the new nuclear suppressor mutants was characterized by temperature-sensitive growth on non-fermentable carbon sources. This mutant was transformed with a genomic yeast library. Two independent types of DNA clones were isolated which both complemented the temperature-sensitive defect. Subcloning and DNA sequencing identified two novel yeast genes which code for proteins with the characteristic features of transcription factors. Both factors exhibit highly structured protein domains consisting of runs and clusters of asparagine and glutamine residues. One of the proteins contains in addition zinc-finger domains of the C2H2-type. Therefore the genes are proposed to be named AZF1 (asparagine-rich **zinc-finger protein**) and PGD1 (polyglutamine domain protein). Gene disruption of both reading frames has no detectable influence on the vegetative growth on complete glucose or glycerol media, indicating that the genes may act as high copy number suppressors of the mutant defect. Additional transformation experiments showed that AZF1 is also an efficient suppressor for the original defect in the core subunit of **mitochondrial** RNA polymerase. The DNA sequences for the AZF1 and PGD1 genes were submitted to the EMBL data base (Accession Numbers: Z26253 and Z26254).

L6 ANSWER 31 OF 36 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1994:420066 BIOSIS

DOCUMENT NUMBER: PREV199497433066

TITLE: Molecular analysis of cytokinin action in
 Physcomitrella patens.

AUTHOR(S): Reski, R.; Kruse, S.; Kasten, B.; Reuter, K.; Wehe,
 M.; Faust, M.; Gorr, G.; Abel, W. O.

CORPORATE SOURCE: Inst. Allgemeine Botanik, D-22609 Hamburg Germany
 SOURCE: Cell Biology International, (1994) Vol. 18, No. 5,
 pp. 539.

Meeting Info.: IVth European Cell Biology Congress
 Prague, Czech Republic June 26-July 1, 1994
 ISSN: 1065-6995.

DOCUMENT TYPE: Conference

LANGUAGE: English

L6 ANSWER 32 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 94245987 EMBASE

DOCUMENT NUMBER: 1994245987

TITLE: A peptide C-terminal to the second Zn finger of human
 vitamin D receptor is able to specify nuclear
 localization.

AUTHOR: Luo Z.; Rouvinen J.; Maenpaa P.H.

CORPORATE SOURCE: Dept. of Biochemistry/Biotechnology, University of
 Kuopio, P. O. B. 1627, FIN-70211 Kuopio, Finland

SOURCE: European Journal of Biochemistry, (1994) 223/2 (381-387).
 ISSN: 0014-2956 CODEN: EJBCAI
 COUNTRY: Germany
 DOCUMENT TYPE: Journal; Article
 FILE SEGMENT: 029 Clinical Biochemistry
 LANGUAGE: English
 SUMMARY LANGUAGE: English
 AB A peptide of 27 amino acids, VDR(102-76), representing residues 76-102 immediately C-terminal to the second Zn finger of human vitamin D receptor (hVDR) was conjugated to fluorescein-labelled IgG using a bifunctional coupling reagent, m-maleimidobenzoyl n-hydroxysuccinimide. Upon microinjection into the cytoplasm of human osteosarcoma MG-63 cells, the chimeras accumulated in the **nuclei**. This transport was arrested by chilling or energy depletion. Two other peptides, VDR(80-67), spanning the N-terminal part of VDR(102-76), and VDR(108-97), spanning the C-terminal part of VDR(102-76), were not able to target the linked proteins to the **nuclei**. SV40(135-112), a peptide containing a well-characterized nuclear localization sequence (amino acids 112-135) of simian virus 40 (SV40) large T-antigen, caused complete nuclear accumulation under the same conditions. **Wheat** germ agglutinin, which inhibits SV40(135-112) transport, also inhibited the nuclear accumulation of VDR(102-76) as did energy depletion.

L6 ANSWER 33 OF 36 SCISEARCH COPYRIGHT 2003 ISI (R)
 ACCESSION NUMBER: 94:319224 SCISEARCH
 THE GENUINE ARTICLE: NL088
 TITLE: PUTATIVE NUCLEAR-LOCALIZATION SIGNALS (NLS) IN PROTEIN TRANSCRIPTION FACTORS
 AUTHOR: BOULIKAS T (Reprint)
 CORPORATE SOURCE: LINUS PAULING INST SCI & MED, 460 PAGE MILL RD, PALO ALTO, CA, 94306 (Reprint)
 COUNTRY OF AUTHOR: USA
 SOURCE: JOURNAL OF CELLULAR BIOCHEMISTRY, (MAY 1994) Vol. 55, No. 1, pp. 32-58.
 ISSN: 0730-2312.
 DOCUMENT TYPE: General Review; Journal
 FILE SEGMENT: LIFE
 LANGUAGE: ENGLISH
 REFERENCE COUNT: 189

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We have recognized about ten distinct forms of strongly basic hexapeptides, containing at least four arginines and lysines, characteristic of nuclear proteins among all eukaryotic species, including yeast, **plants**, flies and mammals. These basic hexapeptides are considered to be different versions of a core nuclear localization signal, NLS. Core NLSs are present in nearly all nuclear proteins and absent from nearly all 'nonassociated' cytoplasmic proteins that have been investigated. We suggest that the few (similar to 10%) protein factors lacking a typical NLS core peptide may enter the **nucleus** via their strong crosscomplexation with their protein factor partners that possess a core NLS. Those cytoplasmic proteins found to possess a NLS-like peptide are either tightly associated with **cell** membrane proteins or are integral components of large cytoplasmic protein complexes. On the other hand, some versions of core NLSs are found

in many cell membrane proteins and secreted proteins. It is hypothesized that in these cases the N-terminal hydrophobic signal peptide of extracellular proteins and the internal hydrophobic domains of transmembrane proteins are stronger determinants for their subcellular localization. The position of core NLSs among homologous nuclear proteins may or may not be conserved; however, if lost from an homologous site it appears elsewhere in the protein.

This search provides a set of rules to our understanding of the nature of core nuclear localization signals: (1) Core NLS are proposed to consist most frequently of an hexapeptide with 4 arginines and lysines; (2) aspartic and glutamic acid residues as well as bulky amino acids (F, Y, W) need not to be present in this hexapeptide; (3) acidic residues and proline or glycine that break the alpha-helix are frequently in the flanking region of this hexapeptide stretch; (4) hydrophobic residues ought not to be present in the core NLS flanking region allowing for the NLS to be exposed on the protein. In this study we attempt to classify putative core NLS from a wealth of nuclear protein transcription factors from diverse species into several categories, and we propose additional core NLS structures yet to be experimentally verified.

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L6 ANSWER 34 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
 ACCESSION NUMBER: 92043906 EMBASE
 DOCUMENT NUMBER: 1992043906
 TITLE: Characterization of a zinc finger DNA-binding protein expressed specifically in Petunia petals and seedlings.
 AUTHOR: Takatsuji H.; Mori M.; Benfey P.N.; Ren L.; Chua N.-H.
 CORPORATE SOURCE: Agrobiological Resource Inst., Tsukuba Science City, Japan
 SOURCE: EMBO Journal, (1992) 11/1 (241-249).
 ISSN: 0261-4189 CODEN: EMJODG
 COUNTRY: United Kingdom
 DOCUMENT TYPE: Journal; Article
 FILE SEGMENT: 022 Human Genetics
 029 Clinical Biochemistry
 LANGUAGE: English
 SUMMARY LANGUAGE: English
 AB In Petunia, the expression of the 5-enolpyruvylshikimate-3-phosphate synthase gene (EPSPS) is tissue-specific and developmentally regulated. Nuclear extracts from Petunia petal contain a factor that interacts with the 5' upstream region of EPSPS. DNase I footprinting experiments revealed four strong binding sites (EP1-EP4) and several weaker sites that appear to bind the same factor. We have isolated a cDNA clone (EPFI) encoding a DNA-binding protein that has similar binding activity to that of the nuclear factor. The deduced amino acid sequence shows that the encoded protein, EPFI, contains two repeats of a Cys2/His2 zinc finger motif. EPFI and the factor detected in nuclear extracts appear to differ in their molecular weight and Zn²⁺ requirements. Nevertheless, Northern blot analyses showed that the expression pattern of EPFI is remarkably similar to that of EPSPS. In addition, as determined by translational fusion of the EPFI upstream region to the .beta.-glucuronidase reporter gene, the cell specific expression pattern of EPFI in flower and seedling is nearly identical to that of EPSPS. Taken together with

the results of cis-element analyses, these observations suggest that EPFI may be one of the factors involved in the activation of EPSPS.

L6 ANSWER 35 OF 36 JICST-EPlus COPYRIGHT 2003 JST

ACCESSION NUMBER: 910803485 JICST-EPlus
 TITLE: Gene Encoding a Putative **Zinc Finger Protein** in *Synechocystis* PCC6803.
 AUTHOR: OGURA Y; YOSHIDA T; NAKAMURA Y; TAKEMURA M; ODA K; OHYAMA K
 CORPORATE SOURCE: Kyoto Univ., Kyoto, JPN
 SOURCE: Agric Biol Chem, (1991) vol. 55, no. 9, pp. 2259-2264. Journal Code: G0021A (Fig. 5, Ref. 22)
 CODEN: ABCHA6; ISSN: 0002-1369
 PUB. COUNTRY: Japan
 DOCUMENT TYPE: Journal; Article
 LANGUAGE: English
 STATUS: New

AB A 5.5-kb Hind III fragment of *Synechocystis* PCC6803 containing a liverwort (ORF316) homolog encoding a putative **zinc finger protein** was cloned. Nucleotide sequence analysis showed that the homology of the amino acid sequence deduced from the ORF326 of *Synechocystis* PCC6803 with the counterparts of a liverwort and **tobacco** was 50% and 46%, respectively. *Synechocystis* ORF326 also showed 38% homology with the dedB gene in *Escherichia coli*. The gene organization of the region in these species of organisms was quite different. This suggests that the *Synechocystis* ORF326 and liverwort ORF316 genes may be related to a common regulatory gene, but not photosynthetic gene characteristic to chloroplasts. (author abst.)

L6 ANSWER 36 OF 36 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 91254811 EMBASE
 DOCUMENT NUMBER: 1991254811
 TITLE: Nuclear location of the 16K non-structural protein of **tobacco** rattle virus.
 AUTHOR: Liu D.H.; Robinson D.J.; Duncan G.H.; Harrison B.D.
 CORPORATE SOURCE: Scottish Crop Research Inst., Invergowrie, Dundee DD2 5DA, United Kingdom
 SOURCE: Journal of General Virology, (1991) 72/8 (1811-1817).
 ISSN: 0022-1317 CODEN: JGVIA Y
 COUNTRY: United Kingdom
 DOCUMENT TYPE: Journal; Article
 FILE SEGMENT: 047 Virology
 LANGUAGE: English
 SUMMARY LANGUAGE: English

AB An antiserum, elicited by a synthetic peptide coupled to bovine serum albumin, reacted specifically with the non-structural 16K protein of **tobacco** rattle virus. The protein was detected in extracts of systemically infected *Nicotiana clevelandii* leaves, but only in those made with the aid of SDS, urea and 2-mercaptoethanol. Immunogold labelling of ultrathin sections showed that the protein was mainly associated with **nuclei**, but was also present in the cytoplasm. These observations suggest that the 16K protein binds to macromolecular components of infected **cells**, especially in **nuclei**, but do not clarify its function.

(FILE 'MEDLINE' ENTERED AT 15:48:31 ON 26 MAR 2003)

L7 4921 SEA FILE=MEDLINE ABB=ON PLU=ON "ZINC FINGERS"/CT
 L8 38235 SEA FILE=MEDLINE ABB=ON PLU=ON PLANTS/CT
 L9 16 SEA FILE=MEDLINE ABB=ON PLU=ON L7 AND L8

L9 ANSWER 1 OF 16 MEDLINE

AN 2001527218 MEDLINE

TI The plant zinc finger protein ZPT2-2 has a unique mode of DNA interaction.

AU Yoshioka K; Fukushima S; Yamazaki T; Yoshida M; Takatsuji H

SO JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Sep 21) 276 (38) 35802-7.
 Journal code: 2985121R. ISSN: 0021-9258.

AB ZPT2-2 is a DNA-binding protein of petunia that contains two canonical TFIIIA-type zinc finger motifs separated by a long linker. We previously reported that ZPT2-2 bound to two separate AGT core sites, with each zinc finger making contact with each core site. Here we present our further characterization of ZPT2-2 by using selected and amplified binding sequence imprinting and surface plasmon resonance analyses; together, these assays revealed some unusual features of the interaction between ZPT2-2 and DNA. These experiments allowed us to conclude that 1) the optimal binding sequence for the N-terminal zinc finger is AGC(T), and that of the C-terminal one is CAGT; 2) multiple arrangements of the two core sites accommodate binding; and 3) the spacing between the two core sites affects the binding affinity. In light of these observations, we propose a new model for the DNA-ZPT2-2 interaction. Further, consistent with this model, a high affinity binding site for ZPT2-2 was found in the promoter region of the ZPT2-2 gene. This site may serve as a cis-element for the autoregulation of ZPT2-2 gene expression.

L9 ANSWER 2 OF 16 MEDLINE

AN 2000028757 MEDLINE

TI Detecting and characterizing gene conversions between multigene family members.

AU Drouin G; Prat F; Ell M; Clarke G D

SO MOLECULAR BIOLOGY AND EVOLUTION, (1999 Oct) 16 (10) 1369-90.
 Journal code: 8501455. ISSN: 0737-4038.

AB We used a variety of methods to detect known gene conversions in the actin gene families of five angiosperm species, the beta-globin gene families of two primate species, and the Zfx/Zfy gene families of seven mammalian species. Our goal was to devise a working strategy which would allow the analysis of the members of a multigene family in order to determine whether there had been gene conversions between its members, identify the genes involved in the gene conversions, establish the lengths of the converted regions, and determine the polarities of the gene conversions. We show that three phylogenetic methods and the homoplasy test of Maynard Smith and Smith perform relatively poorly on our data sets because the sequences we analyzed had large levels of multiple substitutions. The method of Sawyer, the compatibility method of Jakobsen and Easteal, the partition matrix method of Jakobsen, Wilson, and Easteal, and the co-double method of Balding, Nichols, and Hunt can be used to identify the genes which have been involved in gene conversions. The co-double method is more powerful than other methods but requires orthologous sequences from related species. Compatibility, phylogenetic, and nucleotide substitution distribution statistics methods can be used to identify the location

of the converted region(s). Site-by-site compatibility analyses can also be used to identify the direction of the conversion event(s). Combinations of these methods can therefore be used to establish the presence, locations, and polarities of gene conversions between multigene family members.

- L9 ANSWER 3 OF 16 MEDLINE
 AN 1999408259 MEDLINE
 TI Early elicitor induction in members of a novel multigene family coding for highly related RING-H2 proteins in *Arabidopsis thaliana*.
 AU Salinas-Mondragon R E; Garciduenas-Pina C; Guzman P
 SO PLANT MOLECULAR BIOLOGY, (1999 Jul) 40 (4) 579-90.
 Journal code: 9106343. ISSN: 0167-4412.
- AB We describe the identification and structural characterization of a novel family of *Arabidopsis* genes related to ATL2 which encode a variant of the RING zinc finger domain, known as RING-H2. Analysis of genes selected by us and of sequences from *Arabidopsis* stored in databases permitted the prediction of several RING-H2 proteins that contain highly homologous RING domains. The ATL gene family is represented by fifteen sequences that contain, in addition to the RING, a transmembrane domain which is located in most of them towards the N-terminal end. Transgenic *Arabidopsis* seedlings carrying the ATL2 promoter fused to the GUS reporter gene revealed that the expression of ATL2 is rapidly induced after exposure to chitin or inactivated crude cellulase preparations. Rapid induction of transcript accumulation of another member of the ATL family was also observed under the same conditions. These results suggest that some ATLs may be involved in the early stages of the defense response triggered in plants in response to pathogen attack.
- L9 ANSWER 4 OF 16 MEDLINE
 AN 1999320820 MEDLINE
 TI Nuclear factors GT-1 and 3AF1 interact with multiple sequences within the promoter of the Tdc gene from Madagascar periwinkle: GT-1 is involved in UV light-induced expression.
 AU Ouwerkerk P B; Trimborn T O; Hilliou F; Memelink J
 SO MOLECULAR AND GENERAL GENETICS, (1999 Jun) 261 (4-5) 610-22.
 Journal code: 0125036. ISSN: 0026-8925.
- AB Plant secondary metabolites of the terpenoid indole alkaloid (TIA) class comprise several compounds with pharmaceutical applications. A key step in the TIA biosynthetic pathway is catalysed by the enzyme tryptophan decarboxylase (TDC), which channels the primary metabolite tryptophan into TIA metabolism. In *Catharanthus roseus* (Madagascar periwinkle), the Tdc gene is expressed throughout plant development. Moreover, Tdc gene expression is induced by external stress signals, such as fungal elicitor and UV light. In a previous study of Tdc promoter architecture in transgenic tobacco it was shown that the -538 to -112 region is a quantitative determinant for the expression level in different plant organs. Within this sequence one particular region (-160 to -99) was identified as the major contributor to basal expression and another region (-99 to -37) was shown to be required for induction by fungal elicitor. Here, the *in vitro* binding of nuclear factors to the -572 to -37 region is described. In extracts from tobacco and *C. roseus*, two binding activities were detected that could be identified as the previously described nuclear factors GT-1 and 3AF1, based on their mobility and binding characteristics. Both factors appeared to interact with multiple regions in the Tdc promoter. Mutagenesis of GT-1 binding

processes and interaction with target DNA sequences.

- L9 ANSWER 7 OF 16 MEDLINE
 AN 1998280205 MEDLINE
 TI Dof proteins: involvement of transcription factors with a novel DNA-binding domain in tissue-specific and signal-responsive gene expression.
 AU Yanagisawa S
 SO SEIKAGAKU. JOURNAL OF JAPANESE BIOCHEMICAL SOCIETY, (1998 Apr) 70 (4) 280-5. Ref: 12
 Journal code: 0413564. ISSN: 0037-1017.
- L9 ANSWER 8 OF 16 MEDLINE
 AN 1998083196 MEDLINE
 TI Cys2/His2 zinc-finger protein family of petunia: evolution and general mechanism of target-sequence recognition.
 AU Kubo K i; Sakamoto A; Kobayashi A; Rybka Z; Kanno Y; Nakagawa H; Takatsuji H
 SO NUCLEIC ACIDS RESEARCH, (1998 Jan 15) 26 (2) 608-15.
 Journal code: 0411011. ISSN: 0305-1048.
 AB The EPF family is a group of Cys2/His2 zinc-finger proteins in petunia. In these proteins, characteristically long spacer regions have been found to separate the zinc fingers. Our previous DNA-binding studies demonstrated that two-fingered proteins (ZPT2-1 and ZPT2-2), which have spacers of different lengths, bind to two separate AGT core motifs in a spacing specific manner. To investigate the possibility that these proteins might distinguish between the target sequences on the basis of spacing between the core motifs, we screened petunia cDNA library for other proteins belonging to this family. Initial screening by PCR and subsequent cloning of full-length cDNAs allowed us to identify the genes for 10 new proteins that had two, three or four zinc fingers. Among the two-fingered proteins the spacing between zinc fingers varied from 19 to 65 amino acids. The variation in the length of spacers was even more extensive in three- and four-fingered proteins. The presence of such proteins is consistent with our hypothesis that the spacing between the core motifs might be important for target sequence recognition. Furthermore, comparison of diverse protein structures suggests that three- and two-fingered proteins might have resulted due to successive loss of fingers from a four-fingered protein during molecular evolution. We also demonstrate that a highly conserved motif (QALGGH) among the members of EPF family and other Cys2/His2 zinc-finger proteins in plants is critical for the DNA-binding activity.
- L9 ANSWER 9 OF 16 MEDLINE
 AN 96402609 MEDLINE
 TI ZZ and TAZ: new putative zinc fingers in dystrophin and other proteins.
 AU Ponting C P; Blake D J; Davies K E; Kendrick-Jones J; Winder S J
 SO TRENDS IN BIOCHEMICAL SCIENCES, (1996 Jan) 21 (1) 11-13. Ref: 20
 Journal code: 7610674. ISSN: 0968-0004.
- L9 ANSWER 10 OF 16 MEDLINE
 AN 96280737 MEDLINE
 TI A single amino acid determines the specificity for the target sequence of two zinc-finger proteins in plants.
 AU Takatsuji H

- SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1996 Jul 5)
224 (1) 219-23.
Journal code: 0372516. ISSN: 0006-291X.
- AB The EPF family is a group of DNA-binding proteins with two canonical Cys2/His2 zinc-finger motifs in *Petunia*. These proteins are unique in terms of structure in that (i) the two zinc fingers are separated by spacers of various lengths and (ii) the sequence QALGGH is strongly conserved in the zinc-finger motifs of members of the family. In this study, domain-swapping and site-directed mutagenesis experiments with two members of the protein family, EPF2-5 and EPF2-7, which have different target sequences, revealed that only a single amino acid in the second zinc finger is responsible for the difference in target specificity. The position of this amino acid is different from those of determinants of target-sequence specificity in other zinc-finger proteins. Thus, the EPF family recognizes target sequences in a unique manner, together with the recognition of spacings in the target sequence that we demonstrated recently.
- L9 ANSWER 11 OF 16 MEDLINE
AN 95288372 MEDLINE
TI PZF, a cDNA isolated from *Lotus japonicus* and soybean root nodule libraries, encodes a new plant member of the RING-finger family of zinc-binding proteins.
AU Schauser L; Christensen L; Borg S; Poulsen C
SO PLANT PHYSIOLOGY, (1995 Apr) 107 (4) 1457-8.
Journal code: 0401224. ISSN: 0032-0889.
- L9 ANSWER 12 OF 16 MEDLINE
AN 94348284 MEDLINE
TI A new family of zinc finger proteins in *petunia*: structure, DNA sequence recognition, and floral organ-specific expression.
AU Takatsuji H; Nakamura N; Katsumoto Y
SO PLANT CELL, (1994 Jul) 6 (7) 947-58.
Journal code: 9208688. ISSN: 1040-4651.
- AB We have previously cloned a gene for a zinc finger protein (EPF1) that is expressed specifically in petals and interacts with the promoter region of the 5-enolpyruvylshikimate-3-phosphate synthase gene in *petunia*. In an attempt to isolate genes encoding additional factors that interact with this promoter, we cloned four novel genes encoding zinc finger proteins (EPF2-5a, EPF2-5b, EPF2-4, and EPF2-7). Sequence analyses revealed that overall similarity between the EPF1 and the EPF2 protein family, except in the zinc finger motifs and the basic amino acid cluster, was very low, suggesting that the two groups belong to different subfamilies. DNA binding specificities of EPF1, EPF2-5, and EPF2-4 were very similar, as expected from the conserved zinc finger motifs. However, EPF2-7 showed no binding to the probes tested in spite of having the conserved motifs. DNA binding studies using a series of spacing mutant probes suggested a binding mechanism in which the EPF proteins recognize spacings in target DNA. RNA gel blot analyses and histochemical analyses with a promoter and beta-glucuronidase fusion revealed that expression of the EPF2-5 gene (EPF2-5) was petal and stamen specific. Expression of the EPF2-7 gene (EPF2-7) was sepal and petal specific and localized in vascular tissues. The preferential expression in two adjacent floral organs raises the possibility that these genes are downstream transcription factors of floral homeotic genes.

- L9 ANSWER 13 OF 16 MEDLINE
 AN 93383550 MEDLINE
 TI The ribonuclease activity of the two synthetic polypeptides having zinc finger sequence.
 AU Giel M; Rekowski P; Kupryszewski G; Barciszewski J
 SO ACTA BIOCHIMICA POLONICA, (1993) 40 (1) 32-4.
 Journal code: 14520300R. ISSN: 0001-527X.
- L9 ANSWER 14 OF 16 MEDLINE
 AN 93099228 MEDLINE
 TI Putative zinc finger protein encoded by a conserved chloroplast gene is very likely a subunit of a biotin-dependent carboxylase.
 AU Li S J; Cronan J E Jr
 SO PLANT MOLECULAR BIOLOGY, (1992 Dec) 20 (5) 759-61.
 Journal code: 9106343. ISSN: 0167-4412.
- L9 ANSWER 15 OF 16 MEDLINE
 AN 93008359 MEDLINE
 TI The plastome-encoded zfpA gene of a moss contains procaryotic as well as eucaryotic promoter consensus sequences and its RNA abundance is modulated by cytokinin.
 AU Kasten B; Wehe M; Kruse S; Reutter K; Abel W O; Reski R
 SO CURRENT GENETICS, (1992 Oct) 22 (4) 327-33.
 Journal code: 8004904. ISSN: 0172-8083.
 AB Plastid DNA of the moss *Physcomitrella patens* has been sequenced. An open reading frame (ORF 315) was identified downstream from *rbcl*, between *trnR*-CCG and *psaI*. This ORF shares homology with *zfpA*, a putative regulatory gene in *Pisum sativum*. The moss ORF is preceded by a Shine-Dalgarno sequence, two plastid promoter consensus sequences, and three TATA boxes. A specific probe detected three transcripts of low abundance in the wild-type moss and a cytokinin-sensitive chloroplast mutant. Steady state levels of *zfpA* transcripts were different in the two genotypes. In mutant protonemata treated with cytokinin, steady state levels of the largest transcript decreased significantly.
- L9 ANSWER 16 OF 16 MEDLINE
 AN 92136434 MEDLINE
 TI NIT2, the nitrogen regulatory protein of *Neurospora crassa*, binds upstream of *nia*, the tomato nitrate reductase gene, in vitro.
 AU Jarai G; Truong H N; Daniel-Vedele F; Marzluf G A
 SO CURRENT GENETICS, (1992 Jan) 21 (1) 37-41.
 Journal code: 8004904. ISSN: 0172-8083.
 AB The *nit-2* gene of *Neurospora crassa* encodes a trans-acting regulatory protein that activates the expression of a number of structural genes which code for nitrogen catabolic enzymes, including nitrate reductase. The NIT2 protein contains a Cys2/Cys2-type zinc-finger DNA-binding domain that recognizes promoter regions of the *Neurospora* nitrogen-related genes. The NIT2 zinc-finger domain/beta-Gal fusion protein was shown to recognize and bind in a specific manner to two upstream fragments of the *nia* gene of *Lycopersicon esculentum* (tomato) in vitro, whereas two mutant NIT2 proteins failed to bind to the same fragments. The dissociation kinetics of the complexes formed between the NIT2 protein and the *Neurospora nit-3* and the tomato *nia* gene promoters were examined; NIT2 binds more strongly to the *nit-3* promoter DNA fragment than it does to fragments derived from the plant nitrate reductase gene itself. The observed specificity of the binding

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suggests the existence of a NIT2-like homolog which regulates the expression of the nitrate assimilation pathway of higher plants.

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L10 14 SEA ABB=ON PLU=ON ZF PROTEIN
L11 0 SEA ABB=ON PLU=ON L10 AND (PLANT OR MAIZE OR CORN OR
CARROT OR TOBACCO OR TOMATO OR POTATO OR BANANA OR
SOYABEAN OR SOYBEAN OR (SOY OR SOYA) (W) BEAN OR PEPPER OR
WHEAT OR RYE OR RICE OR SPINACH)

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
JICST-EPLUS, JAPIO, CABA, AGRICOLA, FSTA, CROPU, CROPB' ENTERED AT
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L12 1 SEA ABB=ON PLU=ON L11
L13 1 SEA ABB=ON PLU=ON L12 NOT L5

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TITLE: Cloning and characterization of two yeast genes
encoding members of the CCCH class of zinc finger
proteins: Zinc finger-mediated impairment of cell
growth.

AUTHOR(S): Thompson, Michael J.; Lai, Wi S.; Taylor, Gregory A.;
Blackshear, Perry J. (1)

CORPORATE SOURCE: (1) Dep. Med., Duke Univ. Med. Cent., Durham, NC
27710 USA

SOURCE: Gene (Amsterdam), (1996) Vol. 174, No. 2, pp.
225-233.
ISSN: 0378-1119.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Members of the CCCH zinc finger (Zf) protein
family have in common two or more repeats of a novel Zf motif
consisting of Cys and His residues in the form Cx-8Cx-5Cx-3H (where
x is a variable amino acid (aa)). We used a degenerate polymerase
chain reaction (PCR) strategy to clone members of this gene family
from *Saccharomyces cerevisiae*. The deduced aa sequences encoded by
these genes, designated CTH1 and CTH2, share 46% overall identity
and 59% similarity, largely due to the two highly conserved Zf
domains. We found readily detectable expression of a 1.4-kb mRNA
encoding Cth1p. The 1.1-kb mRNA encoding Cth2p was barely detectable
under normal growth conditions; however, disruption of CTH1 resulted
in at least a threefold increase in CTH2 mRNA accumulation. No
change in phenotype was detected following disruption of CTH1 and
CTH2, either singly or together. In contrast, overexpression of the
CTH genes or one of the related mammalian genes, tris-tetraprolin
(TTP), caused delayed entry of cell cultures into exponential
growth, and a decrease in final cell density. Removal of the Zf
domain of Cth1p by truncation or deletion completely reversed this
slow growth phenotype, indicating that it was mediated through this
highly conserved structural motif.

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